

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run On: May 15, 2003, 13:23:56 ; Search time 35 Seconds  
(without alignments)  
167.515 Million cell updates/sec

Title: SEQIDL\_MOD  
Perfect score: 197  
Sequence: 1 ANSFLXXLRGSLRXRCIXX.....XXAKXIFEDVDDTLAFWSKH 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002.\*  
1: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.\*  
2: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.\*  
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21: /SID2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.\*  
22: /SID2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.\*  
23: /SID2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	179	90.9	44	20	Modified GLA domain
2	179	90.9	419	22	Human protein C de
3	179	90.9	419	22	Human protein C de
4	179	90.9	419	22	Human protein C de
5	176	89.3	44	20	Modified GLA domain
6	174	88.3	419	22	Human protein C de
7	174	88.3	419	22	Human protein C de
8	174	88.3	419	22	Human protein C de
9	174	88.3	419	22	Human protein C de
10	174	88.3	419	22	Human protein C de

11	173	87.8	44	20	AA18298	Modified GLA domain
12	170	86.3	44	20	AA18299	Modified GLA domain
13	168	85.3	44	20	AA18307	Modified GLA domain
14	168	85.3	44	20	AA18297	Modified GLA domain
15	160	81.2	44	20	AA18309	Human protein C GL
16	160	81.2	44	20	AA18303	Human protein C GL
17	160	81.2	44	22	AA36402	Human protein C ga
18	160	81.2	45	19	AAW75710	Partial human prot
19	160	81.2	415	21	AA156803	Truncated human pr
20	160	81.2	419	14	AA135760	Protein C (PC). H
21	160	81.2	419	19	AAW2753	Primary structure
22	160	81.2	419	22	AAE08625	Human mature wild
23	160	81.2	419	22	AAE08625	Wild-type human pr
24	160	81.2	419	22	AA36894	Human protein C de
25	160	81.2	419	22	AA36896	Human protein C de
26	160	81.2	419	22	AA36897	Human protein C de
27	160	81.2	419	22	AA36898	Human protein C de
28	160	81.2	419	23	AAU9002	Human Protein C zy
29	160	81.2	419	23	AAU9003	Human Protein C zy
30	160	81.2	419	23	AAU9004	Human Protein C zy
31	160	81.2	419	23	AAU9005	Human Protein C zy
32	160	81.2	419	23	AAU9006	Human Protein C zy
33	160	81.2	419	23	AAU9007	Human Protein C zy
34	160	81.2	419	23	AAU9008	Human Protein C zy
35	160	81.2	419	23	AAU9009	Human Protein C zy
36	160	81.2	419	23	AAU9010	Human Protein C zy
37	160	81.2	419	23	AAU9011	Human Protein C zy
38	160	81.2	419	23	AAU9012	Human Protein C zy
39	160	81.2	419	23	AAU9013	Human Protein C zy
40	160	81.2	419	23	AAU9014	Human Protein C zy
41	160	81.2	419	23	AAU9015	Human Protein C zy
42	160	81.2	419	23	AAU9016	Human Protein C zy
43	160	81.2	419	23	AAU9017	Human Protein C zy
44	160	81.2	419	23	AAU9018	Human Protein C zy
45	160	81.2	419	23	AAU9019	Human Protein C zy

ALIGNMENTS

RESULT 1  
AA18300  
ID AA18300 standard; peptide; 44 AA.  
XX  
AC AA18300;  
XX  
DT 17-AUG-1999 (first entry)  
XX  
DE Modified GLA domain of vitamin K-dependent protein.  
XX  
KW GLA domain; mutein; vitamin K-dependent protein; clotting disorder;  
KW therapy.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key  
FT Location/Qualifiers  
FT Misc-difference 1..44  
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"  
XX  
PN WO9920767-A1.  
XX  
PD 29-APR-1999.  
XX  
PF 20-OCT-1998; 98WO-US22152.  
XX  
PR 23-OCT-1997; 97US-0955636.  
XX  
PA (MINU ) UNIV MINNESOTA.  
XX  
PI Neilsstuen GL;  
XX

DR WPI; 1999-288309/24.  
 XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic  
 PT acid domain, useful for treating clotting disorders  
 XX  
 XX Claim 9; Page 79; 86pp; English.  
 XX  
 CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)  
 CC domain. The invention relates to a vitamin K-dependent polypeptide  
 CC comprising a modified GLA domain containing an amino acid substitution  
 CC which enhances membrane binding of the modified polypeptide as compared  
 CC to the native polypeptide. The polypeptide is used to treat a clotting  
 CC disorder by decreasing or increasing clot formation. Modification of the  
 CC GLA domain results in a protein which has enhanced membrane binding  
 CC affinity as compared to the native protein.  
 XX  
 XX Sequence 44 AA;  
 SQ  
 Query Match 90.9%; Score 179; DB 20; Length 44;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-22;  
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ANSFLXLRQGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44  
 DB 1 ANSFLXLRQGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44  
 RESULT 2  
 AAE08630  
 ID AAE08630 standard; Protein; 419 AA.  
 XX  
 AC AAE08630;  
 XX  
 DT 01-NOV-2001 (first entry)  
 XX  
 DE Human protein C derivative #4.  
 XX  
 KW Human; protein C derivative; anticoagulation activity; thrombosis;  
 KW serpin inactivation; acute coronary syndrome; myocardial infarction;  
 KW vascular occlusive disorder; hypercoagulable state; angina; sepsis;  
 KW disseminated intravascular coagulation; DIC; burn; transplantation;  
 KW sickle cell disease; viral haemorrhagic fever; protein C deficiency;  
 KW haemolytic uremic syndrome; acute arterial thrombotic occlusion;  
 KW thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200159084-A1.  
 XX  
 PD 16-AUG-2001.  
 XX  
 PF 02-FEB-2001; 2001WO-US01221.  
 XX  
 PR 11-FEB-2000; 2000US-0181948.  
 PR 14-MAR-2000; 2000US-0189199.  
 XX  
 PA (EIL ) LILLY & CO ELI.  
 XX  
 PI Gerlitz BE, Grinnell BW, Jones BE;  
 XX  
 DR WPI; 2001-514662/56.  
 DR N-PSDB; AAD15228.  
 XX  
 CC Protein C derivative for treating acute coronary syndromes, vascular  
 PT occlusive disorders, thrombotic disorders and sepsis, comprises  
 PT substitutions at specified amino acid positions  
 XX  
 XX Claim 6; Page 50-51; 59pp; English.  
 PS  
 CC The invention relates to human protein C derivatives and nucleic acid  
 CC molecules encoding such derivatives. These derivatives have increased  
 CC anticoagulation activity, resistance to serpin inactivation and  
 CC increased sensitivity to thrombin activation compared to wild type

CC protein C, and retains the biological activity of the wild type human  
 CC protein C. Protein C derivatives are useful in the manufacture of a  
 CC medicament for the treatment of acute coronary syndromes e.g. myocardial  
 CC infarction and unstable angina; and disease states predisposing to  
 CC thrombosis; vascular occlusive disorders and hypercoagulable states e.g.  
 CC disseminated intravascular coagulation (DIC), burns, transplantations,  
 CC thalassaemia, sickle cell disease, viral haemorrhagic fever and  
 CC haemolytic uremic syndrome; sepsis in combination with bacterial  
 CC permeability increasing protein; thrombotic disorders in combination  
 CC with an anti-platelet agent; protein C deficiency; acute arterial  
 CC thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral  
 CC or peripheral arteries or in vascular grafts in combination with a  
 CC thrombolytic agent. Nucleic acid molecules of the invention are useful  
 CC for treating humans with genetically predisposed prothrombotic disorders  
 CC by gene therapy. The present sequence is human protein C derivative.  
 XX  
 XX Sequence 419 AA;  
 SQ  
 Query Match 90.9%; Score 179; DB 22; Length 419;  
 Best Local Similarity 79.5%; Pred. No. 1.4e-21;  
 Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 ANSFLXLRQGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44  
 DB 1 ANSFLXLRQGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44  
 RESULT 3  
 AAB82677  
 ID AAB82677 standard; Protein; 419 AA.  
 XX  
 AC AAB82677;  
 XX  
 DT 15-OCT-2001 (first entry)  
 XX  
 DE Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S).  
 XX  
 KW Protein C; human; coronary syndrome; thrombosis; angina;  
 KW myocardial infarction; vascular occlusive disorder;  
 KW hypercoagulation; sepsis; protein C deficiency; occlusion;  
 KW thromboembolism; stenosis; antibacterial; immunosuppressive;  
 KW thrombolytic; cardiant; antianginal; anticoagulant; therapy;  
 KW mutant; mutein.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH \*Key Location/Qualifiers  
 FT Misc-difference 10 /note= "His in wild-type protein"  
 FT Misc-difference 11 /note= "Ser in wild-type protein"  
 FT Misc-difference 32 /note= "Gln in wild-type protein"  
 FT Misc-difference 33 /note= "Asn in wild-type protein"  
 FT Misc-difference 194 /note= "Leu in wild-type protein"  
 FT Domain 1..45 /note= "Gla domain"  
 FT Disulfide-bond 50..69  
 FT Disulfide-bond 59..64  
 FT Disulfide-bond 80..89  
 FT Disulfide-bond 98..109  
 FT Disulfide-bond 120..133  
 FT Disulfide-bond 141..277  
 FT Disulfide-bond 196..212  
 FT Disulfide-bond 331..345  
 FT Disulfide-bond 356..384  
 FT Cleavage-site 156..157 /note= "cleavage makes a 2-chain inactive  
 FT precursor (155-amino acid light chain  
 FT attached via a disulfide bond to a



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FT Modified-site 20 /note= "gamma-carboxylated"
FT Modified-site 25 /note= "gamma-carboxylated"
FT Modified-site 26 /note= "gamma-carboxylated"
FT Peptide 158..169 /note= "activation peptide; removal activates the 2-chain zymogen"
FT Cleavage-site 169..170 /note= "thrombin cleavage site"
FT Modified-site 29 /note= "N-glycosylated"
FT Modified-site 248 /note= "N-glycosylated"
FT Modified-site 313 /note= "N-glycosylated"
FT Modified-site 329 /note= "N-glycosylated"
XX WO200157193-A2.
XX 09-AUG-2001.
XX 19-JAN-2001; 2001WO-US00020.
XX 02-FEB-2000; 2000US-0179801.
XX 14-MAR-2000; 2000US-0189197.
XX (ELIL ) LILLY & CO ELI.
XX Gerlitz BE, Jones BE;
XX WPI; 2001-496919/54.
XX Novel human protein C derivative for treating, e.g., myocardial
XX infarction, unstable angina, sepsis, thrombotic disorders, acute
XX arterial thrombotic occlusion, and thromboembolism -
XX Claim 6; Page 56-57; 63pp; English.
XX The present sequence is that of a claimed human protein C derivative
XX in which His at position 10 of the wild-type protein C sequence (see
XX AAB82673) is substituted with Gln, Ser at position 11 with Gly, Gln
XX at position 32 with Glu, Asn at position 33 with Asp, Leu at position
XX 194 with Ser, and Thr at position 254 with Ser. It is an example of
XX protein C derivatives of the invention that have at least 2 amino acid
XX substitutions, but which have increased anticoagulant activity and
XX resistance to inactivation by serpins compared with the wild-type
XX protein, while retaining the biological activity of the wild-type
XX protein. A method of producing the derivatives using recombinant
XX DNA methods is claimed. The protein C derivatives are useful for
XX treating coronary syndromes and disease states predisposing to
XX thrombosis (e.g. myocardial infarction and unstable angina),
XX vascular occlusive disorders and hypercoagulable states, sepsis (in
XX combination with bactericidal permeability increasing protein or
XX with tissue factor pathway inhibitor), thrombotic disorders (in
XX combination with an anti-platelet agent or by local delivery through
XX an intracoronary catheter), protein C deficiency, acute arterial
XX thrombotic occlusion, thromboembolism, or stenosis in coronary,
XX cerebral or peripheral arteries or in vascular grafts. Human
XX patients with genetically predisposed prothrombotic disorders may
XX be treated by gene therapy (all claimed).
XX SQ Sequence 419 AA;
XX Query Match 90.9%; Score 179; DB 22; Length 419;
XX Best Local Similarity 79.5%; Pred. No. 1.4e-21;
XX Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX
XX 1 ANSFLXLRQGLSRXCIXXICDFXXAKXIFEDVDVDTLAFWSKH 44
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XX 1 ANSFLXLRQGLSRXCIXXICDFEAKXIFEDVDVDTLAFWSKH 44
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

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RESULT 5
AAV18301
ID AAV18301 standard; peptide; 44 AA.
XX
XX AC AAV18301;
XX
XX DT 17-AUG-1999 (first entry)
XX
XX DE Modified GLA domain of vitamin K-dependent protein.
XX
XX KW GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
XX therapy.
XX
XX OS Homo sapiens.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 1..44 /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
XX FT acid"
XX
XX PN WO9920767-A1.
XX
XX PD 29-APR-1999.
XX
XX PF 20-OCT-1998; 98WO-US22152.
XX
XX PR 23-OCT-1997; 97US-0955636.
XX
XX PA (MINU ) UNIV MINNESOTA.
XX
XX PI Nelsestuen GL;
XX
XX DR WPI; 1999-288309/24.
XX
XX PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX PT acid domain, useful for treating clotting disorders
XX
XX PS Claim 9; Page 82; 86pp; English.
XX
XX CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
XX CC domain. The invention relates to a vitamin K-dependent polypeptide
XX CC comprising a modified GLA domain containing an amino acid substitution
XX CC which enhances membrane binding of the modified polypeptide as compared
XX CC to the native polypeptide. The polypeptide is used to treat a clotting
XX CC disorder by decreasing or increasing clot formation. Modification of the
XX CC GLA domain results in a protein which has enhanced membrane binding
XX CC affinity as compared to the native protein.
XX
XX SQ Sequence 44 AA;
XX Query Match 89.3%; Score 176; DB 20; Length 44;
XX Best Local Similarity 97.7%; Pred. No. 4.1e-22;
XX Matches 43; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ANSFLXLRQGLSRXCIXXICDFXXAKXIFEDVDVDTLAFWSKH 44
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XX 1 ANSFLXLRQGLSRXCIXXICDFXXAKXIFEDVDVDTLAFWSKH 44
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

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RESULT 6
AAE08627
ID AAE08627 standard; Protein; 419 AA.
XX
XX AC AAE08627;
XX
XX DT 01-NOV-2001 (first entry)
XX
XX DE Human protein C derivative #1.
XX
XX KW Human; protein C derivative; anticoagulation activity; thrombosis;

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KW serpin inactivation; acute coronary syndrome; myocardial infarction;  
 KW vascular occlusive disorder; hypercoagulable state; angina; sepsis;  
 KW disseminated intravascular coagulation; DIC; burn; transplantation;  
 KW sickle cell disease; viral haemorrhagic fever; protein C deficiency;  
 KW haemolytic uremic syndrome; acute arterial thrombotic occlusion;  
 KW thromboembolism; prothrombotic disorder; gene therapy; thalassemia.

XX Homo sapiens.

OS WO200159084-A1.

PN 16-AUG-2001.

PD 02-FEB-2001; 2001WO-US01221.

XX 11-FEB-2000; 2000US-0181948.

PR 14-MAR-2000; 2000US-0189199.

XX (ELIL ) LILLY & CO ELI.

PA Gerlitz BE, Grinnell BW, Jones BE;

PI WPI; 2001-514662/56.

DR N-PSDB; AAD15225.

XX Protein C derivative for treating acute coronary syndromes, vascular  
 PT occlusive disorders, thrombotic disorders and sepsis, comprises  
 PT substitutions at specified amino acid positions

PS Claim 3; Page 46-47; 59pp; English.

XX The invention relates to human protein C derivatives and nucleic acid  
 CC molecules encoding such derivatives. These derivatives have increased  
 CC anticoagulation activity, resistance to serpin inactivation and  
 CC increased sensitivity to thrombin activation compared to wild type  
 CC protein C, and retains the biological activity of the wild type human  
 CC protein C. Protein C derivatives are useful in the manufacture of a  
 CC medicament for the treatment of acute coronary syndromes e.g. myocardial  
 CC infarction and unstable angina; and disease states predisposing to  
 CC thrombosis; vascular occlusive disorders and hypercoagulable states e.g.  
 CC disseminated intravascular coagulation (DIC), burns, transplantations,  
 CC thalassemia, sickle cell disease, viral haemorrhagic fever and  
 CC haemolytic uremic syndrome; sepsis in combination with bacterial  
 CC permeability increasing protein; thrombotic disorders in combination  
 CC with an anti-platelet agent; protein C deficiency; acute arterial  
 CC thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral  
 CC or peripheral arteries or in vascular grafts in combination with a  
 CC thrombolytic agent. Nucleic acid molecules of the invention are useful  
 CC for treating humans with genetically predisposed prothrombotic disorders  
 CC by gene therapy. The present sequence is human protein C derivative.

XX Sequence 419 AA;

Query Match 88.3%; Score 174; DB 22; Length 419;

Best Local Similarity 77.3%; Pred. No. 1e-20; Indels 0; Gaps 0;

Matches 34; Conservative 0; Mismatches 10;

QY 1 ANSFLXLLRQGSLLRXICDXXAKXIFEDVDVDTLAFWSKH 44

DB 1 ANSFLLELRHGSLLRERCIEICDFEAKEIFEDVDVDTLAFWSKH 44

RESULT 7

AAE08628

ID AAE08628 standard; Protein; 419 AA.

XX AAE08628;

XX 01-NOV-2001 (first entry)

XX Human protein C derivative #2.

XX Human; protein C derivative; anticoagulation activity; thrombosis;

KW

KW serpin inactivation; acute coronary syndrome; myocardial infarction;  
 KW vascular occlusive disorder; hypercoagulable state; angina; sepsis;  
 KW disseminated intravascular coagulation; DIC; burn; transplantation;  
 KW sickle cell disease; viral haemorrhagic fever; protein C deficiency;  
 KW haemolytic uremic syndrome; acute arterial thrombotic occlusion;  
 KW thromboembolism; prothrombotic disorder; gene therapy; thalassemia.

XX Homo sapiens.

OS WO200159084-A1.

PN 16-AUG-2001.

PD 02-FEB-2001; 2001WO-US01221.

XX 11-FEB-2000; 2000US-0181948.

PR 14-MAR-2000; 2000US-0189199.

XX (ELIL ) LILLY & CO ELI.

PA Gerlitz BE, Grinnell BW, Jones BE;

PI WPI; 2001-514662/56.

DR N-PSDB; AAD15226.

XX Protein C derivative for treating acute coronary syndromes, vascular  
 PT occlusive disorders, thrombotic disorders and sepsis, comprises  
 PT substitutions at specified amino acid positions

PS Claim 4; Page 47-48; 59pp; English.

XX The invention relates to human protein C derivatives and nucleic acid  
 CC molecules encoding such derivatives. These derivatives have increased  
 CC anticoagulation activity, resistance to serpin inactivation and  
 CC increased sensitivity to thrombin activation compared to wild type  
 CC protein C, and retains the biological activity of the wild type human  
 CC protein C. Protein C derivatives are useful in the manufacture of a  
 CC medicament for the treatment of acute coronary syndromes e.g. myocardial  
 CC infarction and unstable angina; and disease states predisposing to  
 CC thrombosis; vascular occlusive disorders and hypercoagulable states e.g.  
 CC disseminated intravascular coagulation (DIC), burns, transplantations,  
 CC thalassemia, sickle cell disease, viral haemorrhagic fever and  
 CC haemolytic uremic syndrome; sepsis in combination with bacterial  
 CC permeability increasing protein; thrombotic disorders in combination  
 CC with an anti-platelet agent; protein C deficiency; acute arterial  
 CC thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral  
 CC or peripheral arteries or in vascular grafts in combination with a  
 CC thrombolytic agent. Nucleic acid molecules of the invention are useful  
 CC for treating humans with genetically predisposed prothrombotic disorders  
 CC by gene therapy. The present sequence is human protein C derivative.

XX Sequence 419 AA;

Query Match 88.3%; Score 174; DB 22; Length 419;

Best Local Similarity 77.3%; Pred. No. 1e-20; Indels 0; Gaps 0;

Matches 34; Conservative 0; Mismatches 10;

QY 1 ANSFLXLLRQGSLLRXICDXXAKXIFEDVDVDTLAFWSKH 44

DB 1 ANSFLLELRHGSLLRERCIEICDFEAKEIFEDVDVDTLAFWSKH 44

RESULT 8

AAE08629

ID AAE08629 standard; Protein; 419 AA.

XX AAE08629;

XX 01-NOV-2001 (first entry)

XX Human protein C derivative #3.

XX Human; protein C derivative; anticoagulation activity; thrombosis;



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XX 02-FEB-2000; 2000US-0179801.
PR 14-MAR-2000; 2000US-0189197.
XX
XX (ELIL ) LILLY & CO ELI.
XX
XX Gerlitz BE, Jones BE;
XX
XX WPI; 2001-496919/54.
DR N-PSDB; AAH26363.
XX
XX Novel human protein C derivative for treating, e.g., myocardial
PT infarction, unstable angina, sepsis, thrombotic disorders, acute
PT arterial thrombotic occlusion, and thromboembolism -
XX
XX Claim 3; Page 52-53; 63pp; English.
XX
XX The present sequence is that of a claimed human protein C
CC derivative in which Ser at amino acid position 11 of the mature
CC wild-type protein C sequence (see AAB82673) is substituted with
CC Gly, Gln at position 32 with Glu, Asn at position 33 with Asp, and
CC Leu at position 194 with Ser. The protein is an example of protein
CC C derivatives of the invention that have at least 2 amino acid
CC substitutions, but which have increased anticoagulant activity and
CC resistance to inactivation by serpins compared with the wild-type
CC protein, while retaining the biological activity of the wild-type
CC protein. A method of producing the derivatives using recombinant
CC DNA methods is claimed. The protein C derivatives are useful for
CC treating coronary syndromes and disease states predisposing to
CC thrombosis (e.g. myocardial infarction and unstable angina),
CC vascular occlusive disorders and hypercoagulable states, sepsis (in
CC combination with bactericidal permeability increasing protein or
CC with tissue factor pathway inhibitor), thrombotic disorders (in
CC combination with an anti-platelet agent or by local delivery through
CC an intracoronary catheter), protein C deficiency, acute arterial
CC thrombotic occlusion, thromboembolism, or stenosis in coronary,
CC cerebral or peripheral arteries or in vascular grafts. Human
CC patients with genetically predisposed prothrombotic disorders may
CC be treated by gene therapy (all claimed).
XX
XX Sequence 419 AA;
XX
XX Query Match 88.3%; Score 174; DB 22; Length 419;
XX Best Local Similarity 77.3%; Pred. No. 1e-20;
XX Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
XX
OY 1 ANSFLXLRQGSIXRXCIXXICDFXXAXXIFEDVDDTLAFWSKH 44
    ||||| || |||| || |||| || ||||| ||||| |||||
DB 1 ANSFLELRHGSLERECIEICDFEAKEIFEDVDDTLAFWSKH 44
    ||||| || |||| || |||| || ||||| ||||| |||||

RESULT 10
ID AAB82676
XX AAB82676 standard; Protein; 419 AA.
XX
XX AAB82676;
XX
XX 15-OCT-2001 (first entry)
XX
XX Human protein C derivative (S11G/Q32E/N33D/L194S/T254S).
XX
XX Protein C; human; coronary syndrome; thrombosis; angina;
KW myocardial infarction; vascular occlusive disorder;
KW hypercoagulability; sepsis; protein C deficiency; occlusion;
KW thromboembolism; stenosis; antibacterial; immunosuppressive;
KW thrombolytic; cardiant; antianginal; anticoagulant; therapy;
KW mutant; muteln.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 11

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FT Misc-difference 32 /note= "Ser in wild-type protein"
FT /note= "Gln in wild-type protein"
FT Misc-difference 33 /note= "Asn in wild-type protein"
FT Misc-difference 194 /note= "Leu in wild-type protein"
FT Misc-difference 254 /note= "Thr in wild-type protein"
FT Domain 1..45 /note= "Gla domain"
FT Disulfide-bond 50..69
FT Disulfide-bond 59..64
FT Disulfide-bond 80..89
FT Disulfide-bond 98..109
FT Disulfide-bond 120..133
FT Disulfide-bond 141..277
FT Disulfide-bond 196..212
FT Disulfide-bond 331..345
FT Disulfide-bond 356..384
FT Cleavage-site 156..157 /note= "cleavage makes a 2-chain inactive
FT precursor (155-amino acid light chain
FT attached via a disulfide bond to a
FT 262-amino acid heavy chain)"
FT
FT Modified-site 6 /note= "gamma-carboxylated"
FT Modified-site 7 /note= "gamma-carboxylated"
FT Modified-site 14 /note= "gamma-carboxylated"
FT Modified-site 16 /note= "gamma-carboxylated"
FT Modified-site 19 /note= "gamma-carboxylated"
FT Modified-site 20 /note= "gamma-carboxylated"
FT Modified-site 25 /note= "gamma-carboxylated"
FT Modified-site 26 /note= "gamma-carboxylated"
FT Peptide 158..169 /note= "gamma-carboxylated"
FT /note= "activation peptide; removal activates the
FT 2-chain zymogen"
FT Cleavage-site 169..170 /note= "thrombin cleavage site"
FT Modified-site 29 /note= "N-glycosylated"
FT Modified-site 248 /note= "N-glycosylated"
FT Modified-site 313 /note= "N-glycosylated"
FT Modified-site 329 /note= "N-glycosylated"
FT /note= "N-glycosylated"
XX WO200157193-A2.
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XX 09-AUG-2001.
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XX 19-JAN-2001; 2001WO-US000020.
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XX 02-FEB-2000; 2000US-0179801.
PR 14-MAR-2000; 2000US-0189197.
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XX (ELIL ) LILLY & CO ELI.
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XX Gerlitz BE, Jones BE;
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XX WPI; 2001-496919/54.
DR N-PSDB; AAH26364.
XX
XX Novel human protein C derivative for treating, e.g., myocardial
PT infarction, unstable angina, sepsis, thrombotic disorders, acute

```

Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders

Claim 7; Page 78; 86pp; English.

This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.

AA	Sequence	44 AA;
AA	Sequence	44 AA;

Query Match	87.8%	Score 173;	DB 20;	Length 44;
Best Local Similarity	97.7%	Pred. No. 1.3e-21;		
Matches 43;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

OY	1	ANSFLXXLRQGSIXRXCIXXICDFXXAKXIFEDVDOTLAFWSKH	44
D6	1	ANSFLXXLRQSIXRXCIXXICDFXXAKXIFEDVDOTLAFWSKH	44

RESULT 12  
AA18299  
ID AA18299 standard; peptide: 44 AA.

AC AAY18299;

DT 17-AUG-1999 (first entry)

DE Modified GLA domain of vitamin K-dependent protein.

[illegible]

KW  
KW  
KW

glutamine, muscle; vitamin K-dependent protein; clotting disorder;  
therapy.

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OS homo sapiens.  
OS Synthetic.

**XX**

FN	key	location/qualifiers
FT	Misc-difference	1..44

/note= "Xaa= gamma-carboxyglutamic acid, or glutamic

XX

FN  
XX  
WC9920767-AI.

PD 29-APR-1999.

20-OCT-1998: 98WO-US22152.

XX

PR 23-OCT-1997; 9705-0933030.  
XX

PA (MINU ) UNIV MINNESOTA.

PT Nestlesien GL:

XX

DR WFL; 1999-288309/24.  
XX

PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic

PT acid domain, useful for treating clotting disorders  
XX

PS Claim` 8; page 78; 86pp; English.

XX 6

CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)  
CC domain. The invention relates to a vitamin K-dependent polypeptide

CC domain: the invention relates to a vitamin K-dependent polypeptide  
CC comprising a modified GLA domain containing an amino acid substitution

CC which enhances membrane binding of the modified polypeptide as compared

CC to the native polypeptide. The polypeptide is used to treat a clotting

CC disorder by decreasing or increasing clot formation. Modification of the

CC GSTA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.

to attribute as compared to the native protein.



```

AAY18297 standard; peptide; 44 AA.
XX AAY18297;
XX AC AAY18297;
XX DT 17-AUG-1999 (first entry)
XX DE Modified GLA domain of vitamin K-dependent protein.
XX DE GLA domain; muten; vitamin K-dependent protein; clotting disorder;
XX KW therapy.
XX KW Homo sapiens.
XX OS Synthetic.
XX XX
XX FT Key Location/Qualifiers
XX FT Misc-difference 1..44 /note= "xaa- gamma-carboxyglutamic acid, or glutamic
FT FT acid"
XX FT
XX WO9920767-A1.
XX PN
XX PD 29-APR-1999.
XX PF 20-OCT-1998; 98WO-US22152.
XX PR 23-OCT-1997; 97US-0955636.
XX PA (MINU ) UNIV MINNESOTA.
XX PI Nelsestuen GL;
XX DR WPI; 1999-288309/24.
XX PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX PT acid domain, useful for treating clotting disorders
XX PS Claim 6; Page 78; 86pp; English.
XX CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
CC CC domain. The invention relates to a vitamin K-dependent polypeptide
CC CC comprising a modified GLA domain containing an amino acid substitution
CC CC which enhances membrane binding of the modified polypeptide as compared
CC CC to the native polypeptide. The polypeptide is used to treat a clotting
CC CC disorder by decreasing or increasing clot formation. Modification of the
CC CC GLA domain results in a protein which has enhanced membrane binding
CC CC affinity as compared to the native protein.
XX SQ Sequence 44 AA;
Query Match 85.3%; Score 168; DB 20; Length 44;
Best Local Similarity 95.5%; Pred. No. 9.1e-21;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps
QY 1 ANSFLXLRGSLRXRCIXXCICDFXXAKXIFEDVDOTLAFWSKH 44
| | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 ANSFLXLRHSSLKRXRCIXXCICDFXXAKXIFEDVDOTLAFWSKH 44
RESULT 15
AAY18309
ID ID AAY18309 standard; peptide; 44 AA.
XX AC AAY18309;
XX XX
XX DT 17-AUG-1999 (first entry)
XX DE Modified GLA domain of vitamin K-dependent protein.
XX DE GLA domain; muten; vitamin K-dependent protein; clotting disorder;
XX KW therapy.
XX KW Homo sapiens.
OS OS

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OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1..44  
 FT /note= "xaa= gamma-carboxyglutamic acid, or glutamic  
 FT acid"  
 FT  
 PN WO9920767-A1.  
 XX  
 XX 29-APR-1999.  
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 XX 20-OCT-1998; 98WO-US22152.  
 XX  
 XX 23-OCT-1997; 97US-0955636.  
 XX  
 XX (MINU ) UNIV MINNESOTA.  
 XX  
 XX Nelstuen GL;  
 XX  
 XX WPI; 1999-288309/24.  
 XX  
 XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic  
 XX acid domain, useful for treating clotting disorders  
 XX  
 XX Disclosure; Page 79-80; 86pp; English.  
 XX  
 XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)  
 XX domain. The invention relates to a vitamin K-dependent polypeptide  
 XX comprising a modified GLA domain containing an amino acid substitution  
 XX which enhances membrane binding of the modified polypeptide as compared  
 XX to the native polypeptide. The polypeptide is used to treat a clotting  
 XX disorder by decreasing or increasing clot formation. Modification of the  
 XX GLA domain results in a protein which has enhanced membrane binding  
 XX affinity as compared to the native protein.  
 XX  
 SQ Sequence 44 AA;  
 Query Match 81.2%; Score 160; DB 20; Length 44;  
 Best Local Similarity 93.2%; Pred. No. 2e-19;  
 Matches 41; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 ANSFLXLRQSLARXCIXICDFXXAKXIFEDVDDTLAFWSKH 44  
 Db 1 ANSFLXLRHSSLARXCIXICDFXXAFXIFEDVDDTLAFWSKH 44

Search completed: May 15, 2003, 13:27:16  
 Job time : 36 secs

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2003, 13:26:07 ; Search time 18 Seconds  
(without alignments)  
234.995 Million cell updates/sec

Title: SEQIDL\_MOD  
Perfect score: 197  
Sequence: 1 ANSFLXLRQGSIXRCIXX.....XXAKXIFEDVDTLAFWSKH 44  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: pir1:\*
- 2: pir2:\*
- 3: pir3:\*
- 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	160	81.2	461	1 KXHU	protein C (activat
2	140	71.1	461	1 JX0210	protein C (activat
3	139	70.6	461	1 SX8994	protein C (activat
4	122	61.9	456	1 KXBO	protein C (activat
5	115	58.4	482	1 EXRT	coagulation factor
6	114	57.9	492	1 EXBO	coagulation factor
7	110	55.8	488	1 EXHU	coagulation factor
8	101	51.3	443	2 I46932	coagulation factor
9	99	50.3	466	1 KF0U7	coagulation factor
10	86.5	43.9	617	2 A35827	thrombin (EC 3.4.2
11	86.5	43.9	618	2 A35827	thrombin (EC 3.4.2
12	86	43.7	475	1 EXCH	coagulation factor
13	85	43.1	407	1 KF0U7	coagulation factor
14	85	43.1	642	2 S53434	plasma protein S p
15	85	43.1	676	1 KXHU	plasma protein S p
16	84	42.6	622	1 TBHU	thrombin (EC 3.4.2
17	81	41.1	646	2 S38819	plasma protein S -
18	80	40.6	452	1 A30351	coagulation factor
19	80	40.6	459	2 JQ0419	coagulation factor
20	80	40.6	461	1 KF0U	coagulation factor
21	80	40.6	675	1 KXBO	plasma protein S p
22	78	39.6	642	2 S53433	plasma protein S p
23	78	39.6	675	1 KXRTS	plasma protein S p
24	73	37.1	416	1 KFBO	coagulation factor
25	72	36.5	625	1 TBBO	thrombin (EC 3.4.2
26	71	36.0	675	1 KXWS	plasma protein S p
27	69.5	35.3	396	1 KXBOZ	plasma protein z -
28	65.5	33.2	422	1 KXHUZ	plasma protein z -
29	65	33.0	673	2 A48089	growth arrest-spec

ALIGNMENTS

RESULT 1

KXHU

protein C (activated) (EC 3.4.21.69) precursor - human  
N;Alternate names: autoprothrombin IIA; plasma protein C  
C;Species: Homo sapiens (man)  
C;Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 16-Jul-1999

C;Accession: A22331; A25426; A21781; A23789; A00927

R;Foster, D.C.; Yoshitake, S.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985

A;Title: The nucleotide sequence of the gene for human protein C.

A;Reference number: A22331; MUID:85270390; PMID:2991887

A;Accession: A22331

A;Molecule type: DNA

A;Residues: 1-461 <POS1>

A;Cross-references: GB:M11228; NID:G190333; PIDN:AAA60166.1; PID:G190334

R;Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.

Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986

A;Title: Evolution and organization of the human protein C gene.

A;Reference number: A25426; MUID:86120978; PMID:3511471

A;Accession: A25426

A;Molecule type: DNA

A;Residues: 1-445, 'L', 446-461 <PLD>

A;Cross-references: GB:M12712; NID:G190330; PIDN:AAA60165.1; PID:G190332

R;Foster, D.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984

A;Title: Characterization of a cDNA coding for human protein C.

A;Reference number: A21781; MUID:84272714; PMID:6589623

A;Accession: A21781

A;Molecule type: mRNA

A;Residues: 'Q', 107-461 <FOS2>

A;Cross-references: GB:K02059; NID:G190322; PIDN:AAA60164.1; PID:G190323

R;Beckmann, R.J.; Schmidt, R.J.; Santerre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G

Nucleic Acids Res. 13, 5233-5247, 1985

A;Title: The structure and evolution of a 461 amino acid human protein C precursor an

A;Reference number: A23789; MUID:85269639; PMID:2991859

A;Accession: A23789

A;Molecule type: mRNA

A;Residues: 1-461 <REC>

A;Cross-references: GB:X02750; NID:G35689; PIDN:CAA26528.1; PID:G763120

R;Miletich, J.P.; Broze Jr., G.J.

J. Biol. Chem. 265, 11397-11404, 1990

A;Title: Beta protein C is not glycosylated at asparagine 329. The rate of translatio

A;Reference number: A44605; MUID:90293094; PMID:1694179

A;Contents: annotation; carbohydrate binding sites; activation peptide

A;Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is

R;Harris, R.J.; Ling, V.T.; Spellman, M.W.

J. Biol. Chem. 267, 5102-5107, 1992

A;Title: O-linked fucose is present in the first epidermal growth factor domain of fa

A;Reference number: A44606; MUID:92184750; PMID:1544894

A;Contents: annotation; beta-hydroxyaspartic acid

C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that

ivation of factor Va is strongly enhanced by complexing with protein S. Protein C als

growth potentiatin  
growth arrest-spec  
probable MAP kinas  
probable MAP kinas  
probable MAP kinas  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
ammonium transport  
mitogen-activated  
VSG expression slt  
protein-tyrosine k  
platelet-derived g  
tyrosine kinase re  
type II site-speci

C;Comment: Protein C is synthesized in the liver as a single chain precursor, which is b/cn, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,  
C;Genetics:  
A;Gene: GDB:PROC  
A;Cross-references: GDB:120317; OMIM:176860  
A;Map position: 2q13-2q21  
A;Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1  
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C;Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding  
F;1-32/Domain: signal sequence #status predicted <SIG>  
F;27-86/Domain: gla domain homology <GLA>  
F;33-42/Domain: propeptide #status predicted <PRO>  
F;43-137/Product: protein C light chain #status predicted <LCH>  
F;92-131/Domain: EGF homology <EG1>  
F;140-175/Domain: EGF homology <EG2>  
F;200-461/Product: protein C heavy chain #status predicted <HCH>  
F;200-211/Domain: activation peptide #status experimental <APT>  
F;212-445/Domain: trypsin homology <TRY>  
F;48,49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status excluded  
F;59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,238-254,373-387,398-426/T  
F;106-111/Disulfide bonds: #status predicted  
F;110/Binding site: carbohydrate (Thr) (covalent) #status absent  
F;113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F;139,290,355/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F;211-212/Cleavage site: Arg-Leu (thrombin) #status experimental  
F;233,299,402/Active site: His, Asp, Ser #status predicted  
F;371/Binding site: carbohydrate (Asn) (covalent) (partial) #status atypical

Query Match 81.2%; Score 160; DB 1: Length 461;  
Best Local Similarity 70.5%; Pred. No. 8.8e-18;  
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANSPFLXLRGGSLRXRCIXXCIXKICDFXXAKXFEDVDDTFLAFWSKH 44  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 43 ANSFLERLISSLERECIEELCDFEEAKEIFQNVDVDTFLAFWSKH 86

RESULT 2  
JX0210  
protein C (activated) (EC 3.4.21.69) precursor - mouse  
N;Alternate names: vitamin K-dependent serine proteinase  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
C;Accession: JX0210  
R;Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.  
J. Biochem. 111, 491-495, 1992  
A;Title: Isolation and characterization of a mouse protein C cDNA.  
A;Reference number: JX0210; MUID:92316897; PMID:1618739  
A;Accession: JX0210  
A;Molecule type: mRNA  
A;Residues: 1-461 <TAD>  
A;Cross-references: GB:D10445; NID:g220385; PIDN:BAA01235.1; PID:g220386  
A;Experimental source: liver  
C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re  
s.  
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam  
F;1-33/Domain: signal sequence #status predicted <SIG>  
F;27-85/Domain: Gla domain homology <GLA>  
F;34-41/Domain: propeptide #status predicted <PRO>  
F;42-196,199-461/Product: protein C #status predicted <PRC>  
F;42-196/Domain: light chain #status predicted <PCL>  
F;91-130/Domain: EGF homology <EG1>  
F;139-174/Domain: EGF homology <EG2>  
F;199-461/Domain: heavy chain #status predicted <PCH>  
F;199-211/Domain: activation peptide #status predicted <ACT>  
F;212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>  
F;212-445/Domain: trypsin homology <TRY>  
F;47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status  
F;112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
F;121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #stat  
F;214,290,355/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;233,299,402/Active site: His, Asp, Ser #status predicted

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Query Match          71.1%; Score 140; DB 1; Length 461;
Best Local Similarity 59.1%; Pred. No. 1.5e-14;
Matches 26; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANSLFXLRQGLRXCIXCXICDFXXAKXIFEDVDDTLAFWSKH 44
      ||||| : ||| | : |||| | : ||||| : ||||| : ||||| :
DB 42 ANSFLEMRPGSLRECMEEICDFEAEQIFQNVEDTLAFWIKY 85

RESULT 3
SI8994
Protein C (activated) (EC 3.4.21.69) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Oct-1999
C:Accession: SI8994; S24312
R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
submitted to the EMBL Data Library, February 1992
A:Description: The cDNA cloning and mRNA expression of rat protein C.
A:Reference number: SI8994
A:Accession: SI8994
A:Status: preliminary
A:Molecule type: mRNA
A:Molecule type: mRNA
A:Cross-references: EMBL:X64336; NID:g56962; PIDN:CAA45617.1; PID:g56963
R:Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
Biochim. Biophys. Acta 1131, 329-332, 1992
A:Title: The cDNA cloning and mRNA expression of rat protein C.
A:Reference number: S24312; MUID:92329550; PMID:1627650
A:Accession: S24312
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <ORA2>
A:Cross-references: EMBL:X64336; NID:g56962; PIDN:CAA45617.1; PID:g56963
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin
C:Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase
F:1-32/Domain: signal sequence #status predicted <SIG>
F:27-85/Domain: Gla domain homology <GLA>
F:33-42/Domain: propeptide #status predicted <PRO>
F:43-461/Product: protein C #status predicted <PRC>
F:91-130/Domain: EGF homology <EG1>
F:139-174/Domain: EGF homology <EG2>
F:213-445/Domain: trypsin homology <TRY>
F:47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu)
F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:121-130,139-150,146-159,161-174,182-320,239-255,373-387,398-426/Disulfide bond
F:215,291,355/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:254,300,402/Active site: His, Asp, Ser #status predicted

Query Match          70.6%; Score 139; DB 1; Length 461;
Best Local Similarity 59.1%; Pred. No. 2.1e-14;
Matches 26; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANSLFXLRQGLRXCIXCXICDFXXAKXIFEDVDDTLAFWSKH 44
      ||||| : ||| | : |||| | : ||||| : ||||| : ||||| :
DB 42 ANSFLEVRAGSLRECMEEICDFEAEQIFQNVEDTLAFWIKY 85

RESULT 4
KXBO
Protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)
N:Alternate names: autoprothrombin IIA; plasma protein C
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Nov-1980 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
C:Accession: A26250; A18385; A18386; A00928
R:Long, G.L.; Balagaje, R.M.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984
A:Title: Cloning and sequence of bovine protein C.
A:Reference number: A26250; MUID:85014826; PMID:6091100
A:Accession: A26250
A:Molecule type: mRNA
A:Residues: 1-456 <LON>
R:Fernlund, P.; Stenflo, J.

```

J. Biol. Chem. 257, 12170-12179, 1982  
A:Title: Amino acid sequence of the light chain of bovine protein C.  
A:Reference number: A18385; MUID:83007325; PMID:6896876  
A:Accession: A18385  
A:Molecule type: protein  
A:Residues: 40-194 <F&R>  
A:Note: 82-Lys was also found  
R:Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.  
Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983  
A:Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.  
A:Reference number: A19316; MUID:83169769; PMID:6572939  
A:Contents: annotation; revision to residue 110  
R:Stenflo, J.; Fernlund, P.  
J. Biol. Chem. 257, 12180-12190, 1982  
A:Title: Amino acid sequence of the heavy chain of bovine protein C.  
A:Reference number: A18386; MUID:83007326; PMID:6896877  
A:Accession: A18386  
A:Molecule type: protein  
A:Residues: 197-454, PV <STP>  
R:Esmon, N.L.; DeBault, L.E.; Esmon, C.T.  
J. Biol. Chem. 258, 5548-5553, 1983  
A:Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless F  
A:Reference number: A37541; MUID:83213513; PMID:6304092  
A:Contents: annotation; activation; calcium binding  
R:Johnson, A.E.; Esmon, N.L.; Laue, T.M.; Esmon, C.T.  
J. Biol. Chem. 258, 5554-5560, 1983  
A:Title: Structural changes required for activation of protein C are induced by Ca2+ bin  
A:Reference number: A37542; MUID:83213514; PMID:6406503  
A:Contents: annotation; activation; calcium binding  
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re  
B.  
C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is d  
bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reacti  
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro  
cognition of the thrombin-thrombomodulin complex  
C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin  
C:Superfamily: coagulation factor X; EGF homology  
F:1-29/Domain: signal sequence (fragment) #status predicted <SIG>  
F:24-83/Domain: Gla domain homology <GLA>  
F:30-39/Domain: propeptide #status predicted <PRO>  
F:40-194/Product: protein C light chain #status experimental <LCH>  
F:98-128/Domain: EGF homology <EG1>  
F:137-172/Domain: EGF homology <EG2>  
F:197-456/Product: protein C heavy chain #status experimental <HCH>  
F:211-440/Domain: activation peptide #status experimental <APT>  
F:45-46, 53-55, 58-59, 62-64, 65-68, 74/Modified site: gamma-carboxyglutamic acid (Glu) #stat  
F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F:119-128, 137-148, 144-157, 159-172, 180-318, 237-253, 368-382, 393-421/Disulfide bonds: #stat  
F:136, 289, 350/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:252, 298, 397/Active site: His, Asp, Ser #status predicted  
F:366/Binding site: carboxylate (Asn) (covalent) #status predicted  
Query Match 61.9%; Score 122; DB 1; Length 456;  
Best Local Similarity 50.0%; Pred. No. 1.2e-11;  
Matches 21; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
QY 1 ANSFLXLLRQGLXRXICIXXICDXXKXIFEDVDVDTLAFWS 42  
DB 40 ANSFLELRPNVERECSEVCEFEAREIFONTEDTMAFWS 81  
RESULT 5  
EXRNT  
coagulation factor Xa (EC 3.4.21.6) precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 31-Jan-1995 #sequence\_revision 07-Feb-1997 #text\_change 08-Dec-2000  
A:Accession: S49075; JC4670; PS0191; PS0190; I62745  
R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.  
Thromb. Res. 80, 63-73, 1995  
A:Title: Evidence for competition between vitamin K-dependent clotting factors for intra  
A:Reference number: A58498; MUID:96093366; PMID:8578539

A:Accession: S49075  
A:Molecule type: mRNA  
A:Residues: 1-482 <STAL>  
A:Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601  
A:Note: submitted to the EMBL Data Library, June 1994  
R:Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.  
Gene 169, 269-273, 1996  
A:Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.  
A:Reference number: JC4670; MUID:96194815; PMID:8647460  
A:Accession: JC4670  
A:Molecule type: mRNA  
A:Residues: 1-482 <STA2>  
A:Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601  
A:Experimental source: Cos-1 cell  
R:Enjyoji, K.; Miyazaki, K.; Kato, H.  
J. Biochem. 109, 890-898, 1991  
A:Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat  
A:Reference number: PS0190; MUID:92041742; PMID:1718949  
A:Accession: PS0191  
A:Molecule type: protein  
A:Residues: 41-58, 'X', 60-65 <ENJ1>  
A:Accession: PS0190  
A:Molecule type: protein  
A:Residues: 183-186, 'X', 188-207 <ENJ2>  
R:Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.  
Eur. J. Haematol. 52, 162-168, 1994  
A:Title: Analysis of the partial nucleotide sequences and deduced primary structures  
A:Reference number: I46196; MUID:94222160; PMID:8168596  
A:Accession: I62745  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 295-383, 'G', 385-455 <MUR>  
A:Cross-references: GB:D21215; NID:g415309; PIDN:BA04756.1; PID:g455396  
C:Function:  
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the  
A:Pathway: blood coagulation  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-40/Domain: propeptide #status predicted <PRO>  
F:25-84/Domain: Gla domain homology <GLA>  
F:41-179/Product: coagulation factor X light chain #status predicted <LCH>  
F:90-121/Domain: EGF homology <EG1>  
F:129-164/Domain: EGF homology <EG2>  
F:183-483/Product: coagulation peptide #status predicted <APT>  
F:183-231/Domain: activation peptide #status predicted <ACT>  
F:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>  
F:232-460/Domain: trypsin homology <TRY>  
F:46-47, 54, 56, 59, 60, 65, 66, 69, 72, 79/Modified site: gamma-carboxyglutamic acid (Glu) #8  
F:57-62, 90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-340, 238-243, 259-275, 388-402  
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
F:187/Binding site: carboxylate (Thr) (covalent) #status experimental  
F:208/Binding site: carboxylate (Thr) (covalent) #status predicted  
F:218/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:231-232/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #8  
F:274, 320, 417/Active site: His, Asp, Ser #status predicted  
Query Match 58.4%; Score 115; DB 1; Length 482;  
Best Local Similarity 43.2%; Pred. No. 1.7e-10;  
Matches 19; Conservative 10; Mismatches 15; Indels 0; Gaps 0;  
QY 1 ANSFLXLLRQGLXRXICIXXICDXXKXIFEDVDVDTLAFWSKH 44  
DB 41 ANSFEEIKKGNLRCVCEICSEFEAREVFEDEKTEFNKY 84  
RESULT 6  
EXBO  
coagulation factor Xa (EC 3.4.21.6) precursor - bovine  
N:Alternate names: Stuart factor  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 24-Apr-1984 #sequence\_revision 17-Mar-1987 #text\_change 16-Jul-1999

C:Function:

A;A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of calcium ions.

A;Pathway: blood coagulation

C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homologous

C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic acid

F;1-15/Domain: signal sequence #status predicted <SIG>

F;16-40/Domain: propeptide #status predicted <PRO>

F;25-84/Domain: Gla domain homology <GLA>

F;41-180/Product: coagulation factor X light chain #status experimental <LCH>

F;90-121/Domain: EGF homology <EG1>

F;129-164/Domain: EGF homology <EG2>

F;183-492/Product: coagulation factor X heavy chain #status experimental <HCH>

F;183-233/Domain: activation peptide #status experimental <APT>

F;234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>

F;234-461/Domain: trypsin homology <TRY>

F;46, 47, 54, 56, 59, 60, 65, 66, 69, 72, 75, 79/Modified site: gamma-carboxyglutamic acid (Glu)

F;57-62, 90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-341/Disulfide bonds: #status experimental

F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F;200/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental

F;208, 485/Binding site: carbohydrate (Thr) (covalent) #status experimental

F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;233-234/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #status experimental

F;240-245, 260-278, 389-403, 414-442/Disulfide bonds: #status experimental

F;275, 321, 418/Active site: His, Asp, Ser #status predicted

Query Match 57.9%; Score 114; DB 1; Length 492;  
Best Local Similarity 45.5%; Pred. No. 2.5e-10;  
Matches 20; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANSFLXXLRGSLXRCIXICDFXAKXIFEDVDDTLAFWSKH 44  
||||| :||| | | | | | : ||| | | |||  
Db 41 ANSFLEEVKGNLERECLEACSLSEAEVFDEAQTFEWSKY 84

RESULT 7

EXHU

coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human

N;Alternate names: Stuart factor

C;Species: Homo sapiens (man)

C;Date: 15-Nov-1984 #sequence-revision 02-May-1994 #text-change 08-Dec-2000

C;Accession: A24478; JQ0917; A42485; A25853; A2208; A21284; A20362; S39415; I54051;

R;Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.  
Biochemistry 25, 5098-5102, 1986

A;Title: Gene for human Factor X: a blood coagulation factor whose gene organization

A;Reference number: A24478; UID:87026600; PMID:3768336

A;Accession: A24478

A;Molecule type: DNA

A;Residues: 1-488 <LEY>

A;Cross-references: GB:I29433; GB:M14327; NID:g459809; PIDN:AAA52764.1; PID:g182831

R;Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.  
Gene 99, 291-294, 1991

A;Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human c

A;Reference number: JQ0917; UID:91216473; PMID:1902434

A;Accession: JQ0917

A;Molecule type: mRNA

A;Residues: 1-488 <MES>

A;Cross-references: GB:M57285; NID:g182389; PIDN:AAA52421.1; PID:g182390

R;Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.  
J. Biol. Chem. 267, 7395-7401, 1992

A;Title: Liver-specific expression of the gene coding for human factor X, a blood coa

A;Reference number: A42485; UID:92218390; PMID:1313796

A;Accession: A42485

A;Molecule type: DNA

A;Residues: 1-15 <MIA>

A;Experimental source: liver

A;Note: sequence extracted from NCBI backbone (NCBIN:93780, NCBIP:93787)

R;Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.  
Gene 41, 311-314, 1986

A;Title: Isolation and characterization of human blood-coagulation factor X cdna.

A;Reference number: A25853; UID:86221713; PMID:3011603

A;Accession: A25853

A;Molecule type: mRNA

A;Residues: 19-284, 'ER', 289-488 <KAU>

A:Cross-references: GB:M22613; NID:gl80335; PIDN:AAA51984.1; PID:gl80336  
 R:Funf, M.R.; Hay, C.W.; Macgillivray, R.P.A.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985  
 A:Title: Characterization of an almost full-length cDNA coding for human blood coagulation factor VIIa  
 A:Reference number: A22208; MUID:85216545; PMID:2582420  
 A:Accession: A22208  
 A:Molecule type: mRNA  
 A:Residues: 13-441, S', 443-488 <FUN>  
 A:Cross-references: GB:K03194; NID:gl82840; PIDN:AAA52490.1; PID:gl82841  
 R:Kleytus, S.P.; Chung, D.W.; Kistiel, W.; Kurachi, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984  
 A:Title: Characterization of a cDNA coding for human factor X  
 A:Reference number: A21284; MUID:84222026; PMID:6587384  
 A:Accession: A21284  
 A:Molecule type: mRNA  
 A:Residues: 13-284, E', 289-488 <LE2>  
 A:Cross-references: GB:K01886  
 R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weiner  
 Biochemistry 22, 2875-2884, 1983  
 A:Title: Complete amino acid sequence of the light chain of human blood coagulation factor X  
 A:Reference number: A20362; MUID:83257207; PMID:6871167  
 A:Accession: A20362  
 A:Molecule type: protein  
 A:Residues: 41-179 <MCV>  
 R:Inoue, K.; Morita, T.  
 Eur. J. Biochem. 218, 153-163, 1993  
 A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of human factor X  
 A:Reference number: S39414; MUID:94062825; PMID:8243461  
 A:Accession: S39415  
 A:Molecule type: protein  
 A:Residues: 183-234 <INO>  
 A:Note: glycosylation sites  
 A:Note: Identification and characterization of beta-hydroxyaspartic acid  
 R:Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusanam, K.; Lyman, G.  
 Gene 84, 517-519, 1989  
 A:Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human factor X  
 A:Reference number: I54051; MUID:90128299; PMID:2612918  
 A:Accession: I54051  
 A>Status: translation not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-23 <RES>  
 R:Padmanabhan, K.; Padmanabhan, K.P.; Tullinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Blass  
 J. Mol. Biol. 232, 947-966, 1993  
 A:Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.  
 A:Reference number: A49458; MUID:93360277; PMID:8355279  
 A:Contents: annotation; X-ray crystallography, 2.2 angstroms  
 C:Comment: The two chains held together by one disulfide bond are formed from a single-coding gene  
 C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) on the side of the activation peptide  
 C:Genetics:  
 A:Gene: GDB:F10  
 A:Cross-references: GDB:119890; OMIM:227600  
 A:Map position: 13q34-13q34  
 A:Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1  
 A:Note: deficiency of this factor causes Stuart disease  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of factor V  
 A:Pathway: blood coagulation  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-40/Domain: propeptide #status predicted <PRO>  
 F:25-84/Domain: Gla domain homology <GLA>  
 F:41-179/Product: coagulation factor X light chain #status experimental <LCH>  
 F:90-121/Domain: EGF homology <EG1>  
 F:129-164/Domain: EGF homology <EG2>  
 F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>  
 F:183-234/Domain: activation peptide #status experimental <APT>  
 F:235-468/Product: coagulation factor Xa heavy chain #status experimental <ACT>  
 F:235-462/Domain: trypsin homology <TRY>  
 F:46.47.54.56.59.60.65.66.69.72.79/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted  
 F:57-62/Disulfide bonds: #status predicted  
 F:90-101.95-110.112-121.129-140.136-149.151-164.172-342.241-246.261-277.390-404.415-443/

F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:199.211/Binding site: carboxylate (Thr) (covalent) #status experimental  
 F:221.231/Binding site: carboxylate (Asn) (covalent) #status experimental  
 F:234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #status experimental  
 F:276.322.419/Active site: His, Asp, Ser #status experimental  
 Query Match 55.8%; Score 110; DB 1; Length 488;  
 Best Local Similarity 43.2%; Pred. No. 1.1e-09;  
 Matches 19; Conservative 9; Mismatches 16; Indels 0; Gaps 0;  
 QY 1 ANSFLXKXRLXRCIXXICDFXXAKXIFEDVDDTLAFWSKH 44  
 DB 41 ANSFLEMKKHLRECEMEETCSYEAREVFEDSDKTNEFWNKY 84  
 RESULT 8  
 I46932  
 coagulation factor VII - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 12-Feb-1999  
 C:Accession: I46932  
 R:Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.  
 Thromb. Res. 69, 231-238, 1993  
 A:Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII  
 A:Reference number: I46932; MUID:93190306; PMID:8383365  
 A:Accession: I46932  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-443 <BRO>  
 A:Cross-references: GB:S56300; NID:q266294; PID:q266295  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol  
 F:24-83/Domain: Gla domain homology <GLA>  
 F:89-120/Domain: EGF homology <EG1>  
 F:130-166/Domain: EGF homology <EG2>  
 F:192-425/Domain: trypsin homology <TRY>  
 Query Match 51.3%; Score 101; DB 2; Length 443;  
 Best Local Similarity 46.3%; Pred. No. 2.8e-08;  
 Matches 19; Conservative 5; Mismatches 17; Indels 0; Gaps 0;  
 QY 1 ANSFLXKXRLXRCIXXICDFXXAKXIFEDVDDTLAFW 41  
 DB 40 ANSFLELRPGSLERCKEELCSFEAREVFQSTERTKQFW 80  
 RESULT 9  
 KFHU7  
 coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human  
 C:Species: Homo sapiens (man)  
 C:Date: 19-May-1989 #sequence\_revision 19-May-1994 #text\_change 08-Dec-2000  
 C:Accession: A28322; A23819; A31186; B31186; S63524  
 R:O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insaley, M.Y.; Hagen, F.S.; M  
 Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987  
 A:Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dep  
 A:Reference number: A28322; MUID:87260948; PMID:3037537  
 A:Accession: A28322  
 A:Molecule type: DNA  
 A:Residues: 1-466 <OHA>  
 A:Cross-references: GB:J02933; NID:gl80333; PIDN:AAA51983.1; PID:gl80334  
 R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart  
 Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986  
 A:Title: Characterization of a cDNA coding for human factor VII.  
 A:Reference number: A23819; MUID:86205965; PMID:3486420  
 A:Accession: A23819  
 A:Molecule type: mRNA  
 A:Residues: 1-466 <HAG>  
 A:Cross-references: GB:M13232; NID:gl82799; PIDN:AAA8040.1; PID:gl82801  
 R:Thim, L.; Bjorn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen,  
 Biochemistry 27, 7785-7793, 1988  
 A:Title: Amino acid sequence and posttranslational modifications of human factor VII-  
 A:Reference number: A90539; MUID:89088153; PMID:3264725  
 A:Accession: A31186  
 A:Molecule type: protein





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Best Local Similarity 42.2%; Pred. No. 8.5e-06;
Matches 19; Conservative 6; Mismatches 19; Indels 1; Gaps 1;

QY 1 ANS-FLXLRQGSIXRXCIXXICDFXXAKXIFEDVDOTLAFWSKH 44
|||||:::|||||:::|||||:::|||||:::|||||:::
DB 44 ANSGFLEELRKGNLRECVCEQSYCEAFEALESQDITDFVNAKY 88
|||||:::|||||:::|||||:::|||||:::|||||:::

RESULT 12
EXCH
coagulation factor Xa (EC 3.4.21.16) precursor - chicken
N:Alternate names: virus-activating proteinase
C:Species: Gallus gallus (chicken)
C:Date: 12-Feb-1993 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999
C:Accession: S15838; S20380; S20381
R:Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Nagai, Y.
FEBS Lett. 283, 281-285, 1991
A:Title: Primary structure of the virus activating protease from chick embryo. Its identification and purification.
A:Reference number: S15838; MUID:91257322; PMID:2044767
A:Accession: S15838
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-475 <SUZ>
A:Cross-references: DDBJ:D00844; NID:g222869; PIDN:BAA00724.1; PID:g222870
R:Gotoh, B.; Yamauchi, F.; Ogasawara, T.; Nagai, Y.
FEBS Lett. 296, 274-278, 1992
A:Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsible for blood coagulation.
A:Reference number: S20380; MUID:92164779; PMID:1537403
A:Accession: S20380
A:Molecule type: protein
A:Residues: 41-55 <GOT>
A:Accession: S20381
A:Molecule type: protein
A:Residues: 241-246, 'X', 248-251, 'X', 253-261 <GOT>
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of calcium
A:Pathway: blood coagulation
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic acid
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-40/Domain: propeptide #status predicted <PRO>
F:25-84/Domain: Gla domain homology <GLA>
F:81-185/Product: coagulation factor X light chain #status experimental <LCH>
F:90-121/Domain: EGF homology <EGF>
F:129-167/Domain: EGF homology <EG2>
F:186-475/Product: coagulation factor X heavy chain #status predicted <HCH>
F:241-475/Product: activation peptide #status predicted <APT>
F:241-468/Domain: trypsin homology <TRY>
F:46-47, 54, 56, 59, 60, 65, 66, 69, 72, 75, 79/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted
F:57-62, 90-101, 95-110, 112-121, 129-140, 136-152, 154-167, 175-348, 347-252, 267-283, 396-410, 421-430/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asn) (covalent) #status predicted
F:196, 207, 228, 285/Binding site: carbohydrate (Asn)
F:282, 328, 425/Active site: His, Asp, Ser #status predicted

Query Match 43.7%; Score 86; DB 1; Length 475;
Best Local Similarity 40.5%; Pred. No. 7.8e-06;
Matches 17; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANSFLXLRQGSIXRXCIXXICDFXXAKXIFEDVDOTLAFWS 42
|||||:::|||||:::|||||:::|||||:::|||||:::
DB 41 ANSGFLEEMKQGNTERCNEERCSKEAREAFEDNKEETFEWN 82
|||||:::|||||:::|||||:::|||||:::|||||:::

RESULT 13
KPB07
coagulation factor VIIa (EC 3.4.21.21) - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999
C:Accession: A31979; C20274
R:Takeya, H.; Kawabata, S.; Nakagawa, S.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.
J. Biol. Chem. 263, 14868-14877, 1988
A:Title: Bovine factor VII. Its purification and complete amino acid sequence.

Best Local Similarity 43.1%; Score 85; DB 1; Length 407;
Query Match 43.1%; Score 85; DB 1; Length 407;
Best Local Similarity 43.1%; Pred. No. 9.7e-06;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANSFLXLRQGSIXRXCIXXICDFXXAKXIFEDVDOTLAFW 41
|||||:::|||||:::|||||:::|||||:::|||||:::
DB 1 ANSGFLELLPGLSRECEELCSFEAHEIFRNEERTQFW 41
|||||:::|||||:::|||||:::|||||:::|||||:::

RESULT 14
S53434
plasma protein S precursor, vitamin K dependent - rhesus macaque (fragment)
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 16-Jul-1999
C:Accession: S53434
R:Greengard, J.S.; Fernandez, J.A.; Radtke, K.P.; Griffin, J.H.
Biochem. J. 305, 397-403, 1995
A:Title: Identification of candidate residues for interaction of protein S with C4b and C3.
A:Reference number: S53433; MUID:95134217; PMID:7832752
A:Accession: S53434
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-642 <GRE>
A:Cross-references: EMBL:L31380
A:Experimental source: tissue type liver
A:Note: the source is designated as rhesus monkey
C:Genetics:
A:Gene: PROS
C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat
F:1-51/Domain: Gla domain homology (fragment) <GLA>
F:1-7/Domain: signal sequence (fragment) #status predicted <SIG>
F:8-642/Product: plasma protein S #status predicted <MAT>
F:87-120/Domain: EGF homology <EG1>
F:127-165/Domain: EGF homology <EG2>

A:Reference number: A31979; MUID:89008362; PMID:3049594
A:Accession: A31979
A:Molecule type: protein
A:Residues: 1-407 <TAK>
R:McMullen, B.A.; Fujikawa, K.; Kistiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor VII.
A:Reference number: A20274; MUID:83308813; PMID:6688526
A:Accession: C20274
A:Molecule type: protein
A:Residues: 58-62, 'X', 64-68 <MCM>
A:Note: the residue designated 'X' was determined to be hydroxyaspartic acid
R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, J.
Biochem. 104, 867-868, 1988
A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factor VII.
A:Reference number: A44556; MUID:89213999; PMID:3149637
A:Contents: annotation
A:Note: structure and location of covalently bound carbohydrate
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the presence of calcium
A:Pathway: blood coagulation extrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic acid
F:1-152/Product: coagulation factor VIIa light chain #status experimental <MAL>
F:1-44/Domain: Gla domain homology (fragment) <GLA>
F:50-81/Domain: EGF homology <EG1>
F:91-127/Domain: EGF homology <EG2>
F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F:153-387/Domain: trypsin homology <TRY>
F:6, 7, 14, 16, 19, 20, 25, 26, 29, 34, 35/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted
F:17-22, 50-61, 55-70, 72-81, 91-102, 98-114, 114-127, 135-262, 159-164, 178-194, 310-329, 340-343/Modified site: carboxyglutamic acid (Asp) (partial) #status experimental
F:52/Binding site: carbohydrate (Ser) (covalent) #status experimental
F:63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental
F:145, 203/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:152-153/Cleavage site: Arg-Ile (coagulation factor VIIa) #status experimental
F:193, 242, 344/Active site: His, Asp, Ser #status predicted
F:290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

```

[illegible]

GenCore version 5.1.4.p5\_4578  
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OM protein - protein search, using sw model

Run on: May 15, 2003, 13:24:16 ; Search time 11 Seconds  
(without alignments)  
165.905 Million cell updates/sec

Title: SEQIDL\_MOD

Perfect score: 197

Sequence: 1 ANSFLXXLRGSLRXKIXX.....XXAKXIFEDVDITLAFWSKH 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	160	81.2	461	1 PRTC_HUMAN	P04070 homo sapien
2	140	71.1	461	1 PRTC_MOUSE	P33587 mus musculus
3	139	70.6	461	1 PRTC_RAT	P31394 rattus norv
4	138	70.1	458	1 PRTC_RABIT	Q28661 oryctolagus
5	123	62.4	459	1 PRTC_PIG	Q9glp2 sus scrofa
6	122	61.9	456	1 PRTC_BOVIN	P00745 bos taurus
7	114	57.9	492	1 FA10_BOVIN	P00743 bos taurus
8	110	55.8	488	1 FA10_HUMAN	P00742 homo sapien
9	107	54.3	231	1 TWG3_HUMAN	Q9bzd7 homo sapien
10	103	52.3	490	1 FA10_RABIT	O19045 oryctolagus
11	101	51.3	444	1 FA7_RABIT	P98139 oryctolagus
12	99	50.3	466	1 FA7_HUMAN	P08709 homo sapien
13	92	46.7	218	1 TWG1_HUMAN	O14668 homo sapien
14	86.5	43.9	617	1 THRB_RAT	P18292 rattus norv
15	86.5	43.9	618	1 THRB_MOUSE	P19221 mus musculus
16	86	43.7	475	1 FA10_CHICK	P25155 gallus gall
17	85	43.1	409	1 FA7_BOVIN	P22457 bos taurus
18	85	43.1	649	1 PRTS_MACMU	Q28520 macaca mula
19	85	43.1	676	1 PRTS_HUMAN	P07225 homo sapien
20	84.5	42.9	226	1 TWG4_HUMAN	Q9bzd6 homo sapien
21	84	42.6	622	1 THRB_HUMAN	P00734 homo sapien
22	82	41.6	376	1 FA10_TROCA	P81428 tropidechis
23	81	41.1	646	1 PRTS_RABIT	P98118 oryctolagus
24	80	40.6	446	1 FA7_MOUSE	P70375 mus musculus
25	80	40.6	452	1 FA9_CANFA	P19540 canis fami
26	80	40.6	459	1 FA9_MOUSE	P16294 mus musculus
27	80	40.6	461	1 FA9_HUMAN	P00740 homo sapien
28	80	40.6	675	1 PRTS_BOVIN	P07224 bos taurus
29	78	39.6	675	1 PRTS_RAT	P53813 rattus norv
30	73	37.1	416	1 FA9_BOVIN	P00741 bos taurus
31	72	36.5	625	1 THRB_BOVIN	P00735 bos taurus
32	71	36.0	675	1 PRTS_MOUSE	Q08761 mus musculus
33	69.5	35.3	396	1 PRTC_BOVIN	P00744 bos taurus

#### RESULT 1

ID	PRTC_HUMAN	STANDARD;	PRT;	461 AA.
AC	P04070; Q16001; Q15190; Q15189;			
DT	01-NOV-1986 (Rel. 03, Created)			
DT	01-NOV-1986 (Rel. 03, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Vitamin-K dependent protein C precursor (EC 3.4.21.69)			
DE	(Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).			
DE	PROC.			
GN	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85270390; PubMed=2991887;			
RA	Poster D.C., Yoshitake S., Davie E.W.;			
RT	"The nucleotide sequence of the gene for human protein C.;"			
RL	Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85269639; PubMed=2991859;			
RA	Beckmann R.J., Schmidt R.J., Santerre R.F., Plutzky J., Crabtree G.R.,			
RA	Long G.L.;			
RT	"The structure and evolution of a 461 amino acid human protein C			
RT	precursor and its messenger RNA, based upon the DNA sequence of			
RT	cloned human liver cDNAs.;"			
RL	Nucleic Acids Res. 13:5233-5247(1985).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86120978; PubMed=3511471;			
RA	Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.;			
RT	"Evolution and organization of the human protein C gene.;"			
RL	Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi O.,			
RA	Nickerson D.A.;			
RL	Submitted (JUN-2001) to the ENBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE OF 106-461 FROM N.A.			
RX	MEDLINE=84272714; PubMed=6589623;			
RA	Foster D.C., Davie E.W.;			
RT	"Characterization of a cDNA coding for human protein C.;"			
RL	Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).			
RN	[6]			
RP	CARBOHYDRATE-LINKAGE SITE ASN-371.			
RX	MEDLINE=90293094; PubMed=1694179;			
RA	Miletich J.P., Broze G.J. Jr.;			
RT	"Beta protein C is not glycosylated at asparagine 329. The rate of			
RT	translation may influence the frequency of usage at asparagine-X-			
RT	cysteine sites.;"			
RL	J. Biol. Chem. 265:11397-11404(1990).			
RN	[7]			

#### ALIGNMENTS

34	65.5	33.2	400	1	PRTC_HUMAN	P22891 homo sapien
35	65	33.0	202	1	TWG2_HUMAN	O14669 homo sapien
36	52	26.4	501	1	MRC1_CANAL	P43068 candida alb
37	50	25.4	363	1	ADK_TOXGO	Q9LWV2 toxoplasma
38	49	24.9	1363	1	VGR3_MOUSE	P35917 mus musculus
39	48	24.4	422	1	SPM1_SCHPO	O92398 schizosacch
40	48	24.4	1235	1	CYA4_TRYBB	Q26721 trypanosoma
41	48	24.4	1298	1	VGR3_HUMAN	P35916 homo sapien
42	47	23.9	244	1	T2E5_ECOLI	P04390 escherichia
43	47	23.9	554	1	DIAB_SALTY	P37450 salmonella
44	47	23.9	1343	1	VGR2_RAT	O08775 rattus norv
45	47	23.9	1348	1	VGR2_COTJA	P52583 coturnix co

RP HYDROXYLATION  
 RX MEDLINE-92184750; PubMed=1544894;  
 RA Harris R.J., Ling V.T., Spellman M.W.;  
 RT "O-linked fucose is present in the first epidermal growth factor  
 RL domain of factor XII but not protein C.";  
 RN J. Biol. Chem. 267:5102-5107(1992).  
 RP [8]  
 RP 3D-STRUCTURE MODELING OF 175-450.  
 RX MEDLINE-94272342; PubMed=8003977;  
 RA Fisher C.L., Greengard J.S., Griffin J.H.;  
 RT "Models of the serine protease domain of the human antithrombotic  
 RL plasma factor activated protein C and its zymogen.";  
 RN Protein Sci. 3:588-599(1994).  
 RP [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.  
 RX MEDLINE-97157472; PubMed=9003757;  
 RA Mather T., Oganessyan V., Hof P., Huber R., Foundling S., Esmon C.,  
 RT Bode W.;  
 RL "The 2.8 A crystal structure of Gla-domainless activated protein C.";  
 RN EMBO J. 15:6822-6831(1996).  
 RP [10]  
 RP REVIEW ON PROC VARIANTS.  
 RX MEDLINE-93190290; PubMed=8446940;  
 RA Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,  
 RL Sala N., Cooper D.N.;  
 RN "Protein C deficiency: a database of mutations. For the Protein C & S  
 Subcommittee of the Scientific and Standardization Committee of the  
 International Society on Thrombosis and Haemostasis.";  
 RL Thromb. Haemost. 69:77-84(1993).  
 RP [11]  
 RP VARIANT CYS-444.  
 RX MEDLINE-87204221; PubMed=2437584;  
 RA Romeo G., Hassan H.J., Staemfli S., Roncuzzi L., Cianetti L.,  
 RL Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,  
 RT Cortese R.;  
 RN "Hereditary thrombophilia: identification of nonsense and missense  
 mutations in the protein C gene.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).  
 RP [12]  
 RP VARIANT TRP-211 (LONDON-1).  
 RX MEDLINE-90098906; PubMed=2602169;  
 RA Grundy C.B., Chitolie A., Talbot S., Bevan D., Kakkar V.V.,  
 RL Cooper D.N.;  
 RN "Protein C London 1: recurrent mutation at Arg-169 (CGG-->TGG) in  
 the protein C gene causing thrombosis.";  
 RL Nucleic Acids Res. 17:10513-10513(1989).  
 RP [13]  
 RP VARIANT CYS-272.  
 RX MEDLINE-91329836; PubMed=1868249;  
 RA Reitsma P.H., Poort S.R., Allaart C.F., Briet E., Bertina R.M.;  
 RL "The spectrum of genetic defects in a panel of 40 Dutch families with  
 symptomatic protein C deficiency type I: heterogeneity and founder  
 effects.";  
 RL Blood 78:890-894(1991).  
 RP [14]  
 RP VARIANTS ALA-62 (VERMONT-1) AND MET-76.  
 RX MEDLINE-92190481; PubMed=1347706;  
 RA Bovill E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer E.,  
 RL Rainville I.R., Long G.L.;  
 RN "Protein C Vermont: symptomatic type II protein C deficiency  
 associated with two GLA domain mutations.";  
 RL Blood 79:1456-1465(1992).  
 RP [15]  
 RP VARIANT ASP-418 (HONG KONG-2).  
 RX MEDLINE-92305321; PubMed=1611081;  
 RA Sugahara Y., Miura O., Yuen P., Aoki N.;  
 RL "Protein C deficiency Hong Kong 1 and 2: hereditary protein C  
 deficiency caused by two mutant alleles, a 5-nucleotide deletion and  
 a missense mutation.";  
 RL Blood 80:126-133(1992).  
 RP [16]  
 RP VARIANT LEU-289.  
 RX MEDLINE-92380660; PubMed=1511988;

RA Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;  
 RT "A novel homozygous missense mutation in the protein C (PROC) gene  
 RL causing recurrent venous thrombosis.";  
 RN Hum. Genet. 89:683-684(1992).  
 RP [17]  
 RP VARIANTS GLN-220 AND TRP-220.  
 RX MEDLINE-92380661; PubMed=1511989;  
 RA Grundy C.B., Schulman S., Tengborn L., Kakkar V.V., Cooper D.N.;  
 RT "Two different missense mutations at Arg 178 of the protein C (PROC)  
 RL gene causing recurrent venous thrombosis.";  
 RN Hum. Genet. 89:685-686(1992).  
 RP [18]  
 RP VARIANT GLN-220.  
 RX MEDLINE-93250852; PubMed=1301959;  
 RA Gandrille S., Vidaud M., Alach M., Alhenc-Gelas M., Fischer A.M.,  
 RL Gouault-Heilman M., Toulon P., Flessinger J.N., Goossens M.;  
 RN "Two novel mutations responsible for hereditary type I protein C  
 deficiency: characterization by denaturing gradient gel  
 electrophoresis.";  
 RL Hum. Mutat. 1:491-500(1992).  
 RP [19]  
 RP VARIANT SER-334.  
 RX MEDLINE-92276939; PubMed=1593215;  
 RA Yamamoto K., Matsushita T., Sugiyama I., Takamatsu J., Iwasaki E.,  
 RL Wada H., Deguchi K., Shirakawa S., Saito H.;  
 RN "Homozygous protein C deficiency: identification of a novel missense  
 mutation that causes impaired secretion of the mutant protein C.";  
 RL J. Lab. Clin. Med. 119:682-689(1992).  
 RP [20]  
 RP VARIANTS TRP-38; CYS-42; HIS-42; GLN-271 AND ASN-294.  
 RX MEDLINE-93313192; PubMed=8324221;  
 RA Gandrille S., Alhenc-Gelas M., Gaussem P., Aillaud M.-F., Dupuy E.,  
 RL Juhan-Vague I., Alach M.;  
 RN "Five novel mutations located in exons III and IX of the protein C  
 gene in patients presenting with defective protein C anticoagulant  
 activity.";  
 RL Blood 82:159-168(1993).  
 RP [21]  
 RP VARIANTS G-14; Q-211; Y-244; Q-253; L-321; C-328; I-385; T-388 AND  
 V-388.  
 RX MEDLINE-93271391; PubMed=8499565;  
 RA Poort S.R., Pabinger-Fasching I., Mannhalter C., Reitsma P.H.,  
 RL Bertina R.M.;  
 RN "Twelve novel and two recurrent mutations in 14 Austrian families  
 with hereditary protein C deficiency.";  
 RL Blood Coagul. Fibrinolysis 4:273-280(1993).  
 RP [22]  
 RP VARIANT TRP-57.  
 RX MEDLINE-93271396; PubMed=8499568;  
 RA Millar D.S., Grundy C.B., Bignell P., Moffat E.H., Martin R.,  
 RL Kakkar V.V., Cooper D.N.;  
 RN "A GLA domain mutation (Arg 15-->Trp) in the protein C (PROC) gene  
 causing type 2 protein C deficiency and recurrent venous  
 thrombosis.";  
 RL Blood Coagul. Fibrinolysis 4:345-347(1993).  
 RP [23]  
 RP VARIANTS R-145; L-210; W-211; T-243; L-321; M-340 AND Y-426.  
 RX MEDLINE-94123239; PubMed=8292730;  
 RA Tsay W., Greengard J.S., Montgomery R.R., McPherson R.A., Fucci J.C.,  
 RL Koerber M.A., Coughlin J., Griffin J.H.;  
 RN "Genetic mutations in ten unrelated American patients with  
 symptomatic type I protein C deficiency.";  
 RL Blood Coagul. Fibrinolysis 4:791-796(1993).  
 RP [24]  
 RP VARIANT SER-423.  
 RX MEDLINE-94001606; PubMed=8398832;  
 RA Marchetti G., Patraccchini P., Gemmati D., Castaman G., Rodeghiero F.,  
 RL Wacey A., Cooper D.N., Tuddenham E.G., Bernardi F.;  
 RN "Symptomatic type II protein C deficiency caused by a missense  
 mutation (Gly 381-->Ser) in the substrate-binding pocket.";  
 RL Br. J. Haematol. 84:285-289(1993).  
 RP [25]  
 RP SEQUENCE OF 43-64 FROM N.A., AND VARIANT GLY-57 (YONAGO).





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FT DISULFID 161 174 BY SIMILARITY.
FT DISULFID 182 320 INTERCHAIN (BY SIMILARITY).
FT DISULFID 239 255 BY SIMILARITY.
FT DISULFID 373 387 BY SIMILARITY.
FT DISULFID 398 426 BY SIMILARITY.
FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 461 AA; 51912 MW; 84ACF93664EDACD5 CRC64;

Query Match 70.6%; Score 139; DB 1; Length 461;
Best Local Similarity 59.1%; Pred. No. 3.9e-16;
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QY 1 ANSFLXLRQGLRXCXICDXXKXIFEDVDVDTLAFNSKH 44
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DB 42 ANSFLXLRQGLRXCXICDXXKXIFEDVDVDTLAFNSKH 85
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RESULT 4
PRTC_RABIT STANDARD; PRT; 458 AA.
AC Q28661;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysis IIA) (Anticoagulant protein C) (Blood coagulation
  factor XIV) (Fragment).
GN PROC.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Shen L., He X., Dahlback B.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIa.
CC -!- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -!- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -!- PTM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -!- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; U49933; AAC92956.1; -
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.

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DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00089; trypsin; 1.
DR Pfam; PF00594; gla; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
FT NON_TER 1 1 BY SIMILARITY.
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FT PROPEP 28 36 BY SIMILARITY.
FT CHAIN 37 458 VITAMIN K-DEPENDENT PROTEIN C.
FT CHAIN 37 192 PROTEIN C LIGHT CHAIN (BY SIMILARITY).
FT CHAIN 195 458 PROTEIN C HEAVY CHAIN (BY SIMILARITY).
FT PEPTIDE 195 209 ACTIVATION PEPTIDE (BY SIMILARITY).
FT SITE 209 210 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
FT DOMAIN 91 126 EGF-LIKE 1.
FT DOMAIN 130 170 EGF-LIKE 2.
FT DOMAIN 210 458 SERINE PROTEASE.
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  (BY SIMILARITY).
FT MOD_RES 43 43 GAMMA-CARBOXYGLUTAMIC ACID
  (BY SIMILARITY).
FT MOD_RES 50 50 GAMMA-CARBOXYGLUTAMIC ACID
  (BY SIMILARITY).
FT MOD_RES 52 52 GAMMA-CARBOXYGLUTAMIC ACID
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FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID
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FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID
  (BY SIMILARITY).
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID
  (BY SIMILARITY).
FT MOD_RES 62 62 GAMMA-CARBOXYGLUTAMIC ACID
  (BY SIMILARITY).
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID
  (BY SIMILARITY).
FT MOD_RES 107 107 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 250 250 CHARGE RELAY SYSTEM.
FT ACT_SITE 296 296 CHARGE RELAY SYSTEM.
FT ACT_SITE 399 399 CHARGE RELAY SYSTEM.
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FT DISULFID 141 154 BY SIMILARITY.
FT DISULFID 156 169 BY SIMILARITY.
FT DISULFID 177 316 INTERCHAIN (BY SIMILARITY).
FT DISULFID 235 251 BY SIMILARITY.
FT DISULFID 370 384 BY SIMILARITY.
FT DISULFID 395 423 BY SIMILARITY.
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 458 AA; 51087 MW; D75A5F990C8F29D7 CRC64;

Query Match 70.1%; Score 138; DB 1; Length 458;
Best Local Similarity 59.1%; Pred. No. 5.7e-16;
Matches 26; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

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QY 1 ANSFLXLRQSLRXKXICDFFXKXKXIFEDVDVDFLAFWSKH 44  
 DB 42 ANSFLXLRQSLRXKXICDFFXKXKXIFEDVDVDFLAFWSKH 85

RESULT 6  
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 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)  
 DE (Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation  
 DE factor XIV) (Fragment).  
 GN PROC.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85014826; PubMed=6091100;  
 RA Long G.L., Balagaje R.M., McGillivray R.T.A.;  
 RT "Cloning and sequencing of liver cDNA coding for bovine protein C.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).  
 RN [2]  
 RP SEQUENCE OF 40-194.  
 RX MEDLINE=83007325; PubMed=6896876;  
 RA Fernlund P., Stenflo J.;  
 RT "Amino acid sequence of the light chain of bovine protein C";  
 RL J. Biol. Chem. 257:12170-12179(1982).  
 RN [3]  
 RP REVISION TO 110.  
 RX MEDLINE=83169769; PubMed=6572939;  
 RA Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;  
 RT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).  
 RN [4]  
 RP SEQUENCE OF 197-456.  
 RX MEDLINE=83007326; PubMed=6896877;  
 RA Stenflo J., Fernlund P.;  
 RT "Amino acid sequence of the heavy chain of bovine protein C";  
 RL J. Biol. Chem. 257:12180-12190(1982).  
 RN [5]  
 RP PROCESSING, AND CALCIUM-BINDING DATA.  
 RX MEDLINE=83213513; PubMed=6304092;  
 RA Esmon N.L., Debault L.E., Esmon C.T.;  
 RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-  
 RT domainless protein C";  
 RL J. Biol. Chem. 258:5548-5553(1983).  
 RN [6]  
 RP PROCESSING, AND CALCIUM-BINDING DATA.  
 RX MEDLINE=83213514; PubMed=6406503;  
 RA Johnson A.E., Esmon N.L., Laue T.M., Esmon C.T.;  
 RT "Structural changes required for activation of protein C are induced  
 RT by Ca2+ binding to a high affinity site that does not contain gamma-  
 RT carboxyglutamic acid";  
 RL J. Biol. Chem. 258:5554-5560(1983).  
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT  
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA  
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va  
 CC and VIIIA.  
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED  
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE  
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A  
 CC TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS  
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS  
 CC STRONGLY PROMOTED BY THROMBOMODULIN.  
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME

CC CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.  
 CC CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING  
 CC CC SITE IS NECESSARY FOR THE RECOGNITION OF THE  
 CC CC THROMBIN-THROMBOMODULIN COMPLEX.  
 CC CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC CC  
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 CC CC EMBL: K02435; AAA30685.1; -  
 CC CC PIR: A00928; KXBO.  
 CC CC HSP: P04070; LPCU.  
 CC CC MEROPS: S01.218; -  
 CC CC InterPro: IPR000152; Asx\_hydroxyl.  
 CC CC InterPro: IPR000561; EGF-like.  
 CC CC InterPro: IPR001881; EGF\_Ca.  
 CC CC InterPro: IPR001254; Ser\_protease\_Try.  
 CC CC InterPro: IPR000294; VitK\_dep\_GLA.  
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 CC CC Pfam: PF00089; trypsin; 1.  
 CC CC Pfam: PF00594; gla; 1.  
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 CC CC PROSITE: PS01186; EGF\_2; 2.  
 CC CC PROSITE: PS01187; EGF\_Ca; 1.  
 CC CC PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
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 CC CC PROSITE: PS00134; TRYPSIN\_HIS; FALSE\_NEG.  
 CC CC PROSITE: PS00135; TRYPSIN\_SER; 1.  
 CC CC KW Blood coagulation; Glycoprotein; Serine protease;  
 CC CC Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
 CC CC EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.  
 CC CC NON\_TER 1  
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 CC CC CHAIN 197 456  
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 CC CC DISULFID 137 148  
 CC CC DISULFID 144 157  
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 CC CC PROTEIN C LIGHT CHAIN.  
 CC CC PROTEIN C HEAVY CHAIN.  
 CC CC ACTIVATION PEPTIDE.  
 CC CC EGF-LIKE 1.  
 CC CC EGF-LIKE 2.  
 CC CC SERINE PROTEASE.  
 CC CC GAMMA-CARBOXYGLUTAMIC ACID.  
 CC CC GAMMA-CARBOXYGLUTAMIC ACID.  
 CC CC GAMMA-CARBOXYGLUTAMIC ACID.  
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 CC CC HYDROXYLATION.  
 CC CC CHARGE RELAY SYSTEM.  
 CC CC CHARGE RELAY SYSTEM.  
 CC CC BY SIMILARITY.  
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FT DISULFID 159 172 BY SIMILARITY.
FT DISULFID 180 318 INTERCHAIN.
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FT DISULFID 368 382
FT DISULFID 393 421
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FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .)
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .)
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .)
FT VARIANT 82 82 F -> K.
FT CONFLICT 455 456 VP -> PV (IN REF. 4).
SQ SEQUENCE 456 AA; 51407 MW; CAAF6833F894C209 CRC64;

Query Match 61.9%; Score 122; DB 1; Length 456;
Best Local Similarity 50.0%; Pred. No. 3.3e-13;
Matches 21; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

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Db 40 ANSFLELRPGNVERECSEVCEFEAREIFQNTDMAFWS 81

RESULT 7
FA10_BOVIN STANDARD; PRT; 492 AA.
AC P00743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 1-487 FROM N.A.
RX MEDLINE=84247315; PubMed=6330671;
Fung M.R., Campbell R.M., McGillivray R.T.A.;
"Blood coagulation factor X mRNA encodes a single polypeptide chain
containing a prepro leader sequence.";
Nucleic Acids Res. 12:4481-4492(1984).
RN [2]
RP SEQUENCE OF 41-180.
RX MEDLINE=80130563; PubMed=6766735;
Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
Titani K.;
"Amino acid sequence of the light chain of bovine factor X1 (Stuart
factor).";
Biochemistry 19:659-667(1980).
RN [3]
RP REVISION TO 103.
RX MEDLINE=83308813; PubMed=6688526;
McMullen B.A., Fujikawa K., Kistel W.;
"The occurrence of beta-hydroxyaspartic acid in the vitamin
K-dependent blood coagulation zymogens.";
Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [4]
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=76053069; PubMed=1059093;
Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
Neurath H.;
"Bovine factor X1 (Stuart factor): amino-acid sequence of heavy
chain.";
Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
RN [5]
RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
Inoue K., Morita T.;
"Identification of O-linked oligosaccharide chains in the activation
peptides of blood coagulation factor X: the role of the carbohydrate
moieties in the activation of factor X.";

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RL Eur. J. Biochem. 218:153-163(1993).
RN [6]
RP ACTIVE SITE.
RX MEDLINE=73053314; PubMed=4264286;
Titani K., Hermodson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
Neurath H., Davie E.W.;
"Bovine factor X 1a (activated Stuart factor). Evidence of homology
with mammalian serine proteases.";
Biochemistry 11:4899-4903(1972).
RN [7]
RP PROCESsing.
RX MEDLINE=76053121; PubMed=1059122;
Fujikawa K., Titani K., Davie E.W.;
"Activation of bovine factor X (Stuart factor): conversion of factor
Xa-alpha to factor Xa-beta.";
Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
RN [8]
RP CALCIUM-BINDING DATA.
RX MEDLINE=84185716; PubMed=6546930;
Sugo T., Björk I., Holmgren A., Stenflo J.;
"Calcium-binding properties of bovine factor X lacking the gamma-
carboxyglutamic acid-containing region.";
J. Biol. Chem. 259:5705-5710(1984).
RN [9]
RP SULFATION.
RX MEDLINE=86140210; PubMed=3949800;
Morita T., Jackson C.M.;
"Localization of the structural difference between bovine blood
coagulation factors XI and X2 to tyrosine 18 in the activation
peptide.";
J. Biol. Chem. 261:4008-4014(1986).
RN [10]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=91084483; PubMed=2261466;
Selander M., Persson E., Stenflo J., Drakenberg T.;
"1H NMR assignment and secondary structure of the Ca2(+)-free form of
the amino-terminal epidermal growth factor like domain in coagulation
factor X.";
Biochemistry 29:8111-8118(1990).
RN [11]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92329412; PubMed=1627540;
Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
Teleman O.;
"Three-dimensional structure of the apo form of the N-terminal
EGF-like module of blood coagulation factor X as determined by NMR
spectroscopy and simulated folding.";
Biochemistry 31:5974-5983(1992).
RN [12]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92406922; PubMed=1527084;
Selander-Sunnerhagen M., Ullner M., Persson E., Teleman O.,
Stenflo J., Drakenberg T.;
"How an epidermal growth factor (EGF)-like domain binds calcium. High
resolution NMR structure of the calcium form of the NH2-terminal EGF-
like domain in coagulation factor X.";
J. Biol. Chem. 267:19642-19649(1992).
RN [13]
RP STRUCTURE BY NMR OF 41-126.
RX MEDLINE=96387194; PubMed=8794734;
Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
Trehwella J.;
"The relative orientation of Gla and EGF domains in coagulation
factor X is altered by Ca2+ binding to the first EGF domain. A
combined NMR-small angle X-ray scattering study.";
Biochemistry 35:11547-11559(1996).
RN CC
-1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
converts prothrombin to thrombin in the presence of factor Va,
calcium and phospholipid during blood clotting.
RN CC
-1- CATALYTIC ACTIVITY: preferential cleavage: Arg-I-Thr and then
Arg-I-Ile bonds in prothrombin to form thrombin.
RN CC
-1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR

```



Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).  
 [7] SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=94062825; PubMed=8243461;  
 RA Inoue K., Morita T.;  
 RT "Identification of O-linked oligosaccharide chains in the activation  
 RT peptides of blood coagulation factor X. The role of the carbohydrate  
 RT moieties in the activation of factor X.";  
 RL Eur. J. Biochem. 218:153-163(1993).  
 RN [8]  
 RP SEQUENCE OF 1-23 FROM N.A.  
 RX MEDLINE=90128299; PubMed=2612918;  
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhushanam K., Lyman G.;  
 RT "Cloning and characterization of the 5' end (exon 1) of the gene  
 RT encoding human factor X.";  
 RL Gene 84:517-519(1989).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=93360277; PubMed=8355279;  
 RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,  
 RA Huber R., Blankenship D.T., Cardin A.D., Kiesel W.;  
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";  
 RL J. Mol. Biol. 232:947-966(1993).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=98283982; PubMed=9618463;  
 RA Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;  
 RT "Structural basis for chemical inhibition of human blood coagulation  
 RT factor Xa.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 CC converts prothrombin to thrombin in the presence of factor Va,  
 CC calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 CC Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 CC MORE DISULFIDE BONDS.  
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -1- PTM: N- AND O-GLYCOSYLATED.  
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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 CC EMBL; K03194; AAA52490.1; -;  
 CC EMBL; M57285; AAA52421.1; -;  
 CC EMBL; L29433; AAA52764.1; -;  
 CC EMBL; L00390; AAA52764.1; JOINED.  
 CC EMBL; L00391; AAA52764.1; JOINED.  
 CC EMBL; L00392; AAA52764.1; JOINED.  
 CC EMBL; L00393; AAA52764.1; JOINED.  
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 CC EMBL; L00396; AAA52764.1; JOINED.  
 CC EMBL; M22613; AAA51984.1; -;  
 CC EMBL; K01886; AAA52486.1; -;  
 CC EMBL; M33297; AAA52636.1; -;  
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 CC PIR; A24478; A24478.  
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DR PDB; 1FAX; 29-OCT-97.  
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 DR PDB; 1XKB; 23-MAR-99.  
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 DR MIM; 134530; -;  
 DR MIM; 227600; -;  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF-2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00089; trypsin; 1.  
 DR Pfam; PF00594; gla; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00001; EGF\_Like; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE; PS02040; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;  
 KW gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 KW Signal; Zymogen; EGF-like domain; Repeat; 3D-structure.  
 FT SIGNAL 1 31  
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 FT CHAIN 41 179  
 FT CHAIN 183 488  
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 FT CHAIN 235 488  
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 FACTOR X LIGHT CHAIN.  
 FACTOR X HEAVY CHAIN.  
 ACTIVATION PEPTIDE.  
 ACTIVATED FACTOR XA, HEAVY CHAIN.  
 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).  
 EGF-LIKE 2.  
 SERINE PROTEASE.  
 GAMMA-CARBOXYGLUTAMIC ACID.  
 GAMMA-CARBOXYGLUTAMIC ACID.  
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 O-LINKED (GLNAC. . .).  
 N-LINKED (GLNAC. . .).  
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 N-LINKED (GLNAC. . .).  
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 CHARGE RELAY SYSTEM.  
 CHARGE RELAY SYSTEM.  
 CHARGE RELAY SYSTEM.

Best Local Similarity 43.2%; Pred. No. 4.2e-11;  
Matches 19; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANSFLXLRGSLRXRCIXXCIDPFXAKXIFEDVDDTLAFWSKH 44  
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Db 41 ANSFLEMKGHLCRECMETCSYEAREVFEDSDKTNEFWKY 84

RESULT 9  
TMG3\_HUMAN STANDARD; PRT; 231 AA.

AC Q9BDJ7  
ID TMG3\_HUMAN  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Transmembrane gamma-carboxyglutamic acid protein 3 precursor.  
GN TMG3  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_Taxid=9606;  
RN [1]  
RZ SEQUENCE FROM N.A.  
RC TISSUE-Spinal cord.  
CX MEDLINE=21117044; PubMed=11171957;  
RT Kulman J.D., Harris J.E., Xie L., Davie E.W.;  
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid  
RT proteins expressed broadly in fetal and adult tissues.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).  
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -|- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.  
CC -|- PTM: Glc residues are produced after subsequent posttranslational  
CC modifications of glutamic acid by a vitamin K-dependent gamma-  
CC carboxylase.  
CC -----  
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CC or send an email to license@isb-sib.ch).

EMBL: AF326350; AAK00955.1; -  
DR HSSP; P00740; 1CFH.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00594; gla\_1.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00069; GLA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.  
FT PROPEP 1 19 POTENTIAL.  
FT CHAIN 20 231 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID  
FT FT FT FT  
FT DOMAIN 20 78 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 79 101 POTENTIAL.  
FT DOMAIN 102 231 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 23 60 GLA-RICH.  
SQ SEQUENCE 231 AA; 25848 MW; 8A373E4848490D81 CRC64;

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QY 1 ANSFLXLRGSLRXRCIXXCIDPFXAKXIFEDVDDTLAFW 41  
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Db 20 ANEFLEEELRGCTIERECMEETCSYEVEKFENKEKTEWF 60

RESULT 10  
FA10\_RABIT STANDARD; PRT; 490 AA.  
ID FA10\_RABIT

KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 FT SIGNAL; Zymogen; EGF-like domain; Repeat.  
 FT 1 20 POTENTIAL.  
 FT PROPEP 21 40 BY SIMILARITY.  
 FT CHAIN 41 180 FACTOR X LIGHT CHAIN.  
 FT CHAIN 184 490 FACTOR X HEAVY CHAIN.  
 FT PROPEP 184 232 ACTIVATION PEPTIDE.  
 FT CHAIN 233 490 ACTIVATED FACTOR XA, HEAVY CHAIN.  
 FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 125 165 EGF-LIKE 2.  
 FT DOMAIN 233 490 SERINE PROTEASE.  
 FT MOD\_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
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 FT SIMILARITY).  
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 FT SIMILARITY).  
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 FT SIMILARITY).  
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 FT SIMILARITY).  
 FT MOD\_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 75 75 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID (BY  
 FT SIMILARITY).  
 FT MOD\_RES 103 103 HYDROXYLATION (BY SIMILARITY).  
 FT ACT\_SITE 274 274 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 320 320 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 417 417 CHARGE RELAY SYSTEM.  
 FT DISULFID 90 101 BY SIMILARITY.  
 FT DISULFID 95 110 BY SIMILARITY.  
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 FT DISULFID 129 140 BY SIMILARITY.  
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 FT DISULFID 151 164 BY SIMILARITY.  
 FT DISULFID 172 340 INTERCHAIN (BY SIMILARITY).  
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 FT DISULFID 259 275 BY SIMILARITY.  
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 FT DISULFID 413 441 BY SIMILARITY.  
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 Matches 19; Conservative 9; Mismatches 16; Indels 0; Gaps 0;  
 QY 1 ANSFLXLRGSLRXICIXXICDFFXXAKXIFEDVDLFAWSKH 44  
 DB 41 ANSFLKKGKGNLERECWEENCSTEALEVFEDREKTNFEWNKY 84  
 RESULT 11  
 ID FA7\_RABIT STANDARD; PRT; 444 AA.  
 AC P98139; P79224;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin  
 conversion accelerator).

GN Oryctolagus cuniculus (Rabbit).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=93190306; PubMed=8383365;  
 RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;  
 RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation  
 factor VII."; Thromb. Res. Suppl. 69:231-238(1993).  
 RL [2]  
 RN REVISION TO 395.  
 RP TISSUE=Liver;  
 RC Ruiz S.R., Blajchman M.A., Clarke B.J.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZMOGEN FORM. FACTOR VII IS  
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR  
 CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR XA  
 CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR IXA  
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO  
 CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY  
 CC SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to  
 CC form factor Xa.  
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED  
 CC BY A DISULFIDE BOND (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: PLASMA.  
 CC -1- PFM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
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 CC -----  
 CC EMBL; U77477; AAB37326.1; -  
 CC HSSP; P08709; 1FAK.  
 CC MEROPS; S01.215; -  
 CC InterPro; IPR000152; Asx\_hydroxyl.  
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 CC InterPro; IPR000561; EGF-like.  
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 CC InterPro; IPR001881; EGF\_Ca.  
 CC InterPro; IPR002383; GLA\_blood.  
 CC InterPro; IPR001254; Ser\_protease\_Try.  
 CC InterPro; IPR000294; VitK\_dep\_GLA.  
 CC Pfam; PF00008; EGF; 2.  
 CC Pfam; PF00089; trypsin; 1.  
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 CC SMART; SM00069; GLA; 1.  
 CC SMART; SM00020; Tryp\_SPC; 1.  
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 CC PROSITE; PS00022; EGF\_1; 1.  
 CC PROSITE; PS01186; EGF\_2; 1.  
 CC PROSITE; PS01187; EGF\_CA; 1.  
 CC PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
 CC PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 CC PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 CC PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;

KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;  
 KW EGF-like domain; Repeat; Signal; Hydroxylation.  
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 FT CHAIN 45 74  
 FT DOMAIN 85 121  
 FT DOMAIN 126 167  
 FT DOMAIN 132 444  
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 FT ACT\_SITE 222 232  
 FT ACT\_SITE 281 281  
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 FT BINDING 377 377  
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 FT DISULFID 130 141  
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 DB 40 ANSFLELRPGSLRECKELCSFEAREVFQSTERTKQFV 80  
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 FA7\_HUMAN  
 ID FA7\_HUMAN STANDARD; PRT; 466 AA.  
 AC P08709; Q14339;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin  
 DE conversion accelerator) (Eptacog alfa).  
 GN F7.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=86205965; PubMed=3486420;  
 RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,  
 RA Woodbury R.G., Hart C.E., Insley M.Y., Kiesel W., Kurachi K.,

RA Davie E.W.;  
 RT "Characterization of a cDNA coding for human factor VII.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87260948; PubMed=3037537;  
 RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,  
 RA Hagen F.S., Murray M.J.;  
 RT "Nucleotide sequence of the gene coding for human factor VII, a  
 RT vitamin K-dependent protein participating in blood coagulation.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.  
 RA Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,  
 RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.  
 RX MEDLINE=89088153; PubMed=3264725;  
 RA Thim L., Bjoern S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,  
 RA Pedersen A.H., Hedner U.;  
 RT "Amino acid sequence and posttranslational modifications of human  
 RT factor VIIa from plasma and transfected baby hamster kidney cells.";  
 RL Biochemistry 27:7785-7793(1988).  
 RN [5]  
 RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.  
 RX MEDLINE=91250411; PubMed=1904059;  
 RA Bjoern S., Foster D.C., Thim L., Wiberg F.C., Christensen M.,  
 RA Komiyama Y., Pedersen A.H., Kiesel W.;  
 RT "Human plasma and recombinant factor VII. Characterization of O-  
 RT glycosylations at serine residues 52 and 60 and effects of site-  
 RT directed mutagenesis of serine 52 to alanine.";  
 RL J. Biol. Chem. 266:11051-11057(1991).  
 RN [6]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.  
 RX MEDLINE=90062160; PubMed=2511201;  
 RA Nishimura H., Kawabata S., Kiesel W., Hase S., Ikenaka T., Takao T.,  
 RA Shimonishi Y., Iwanaga S.;  
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide  
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first  
 RT epidermal growth factor-like domain of human factors VII and IX and  
 RT protein Z and bovine protein Z.";  
 RL J. Biol. Chem. 264:20320-20325(1989).  
 RN [7]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.  
 RX MEDLINE=91344709; PubMed=2129367;  
 RA Iwanaga S., Nishimura H., Kawabata S., Kiesel W., Hase S., Ikenaka T.;  
 RT "A new trisaccharide sugar chain linked to a serine residue in the  
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";  
 RL Adv. Exp. Med. Biol. 281:121-131(1990).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
 RX MEDLINE=96175641; PubMed=8598903;  
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,  
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;  
 RT "The crystal structure of the complex of blood coagulation factor  
 RT VIIa with soluble tissue factor.";  
 RL Nature 380:41-46(1996).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
 RX MEDLINE=99126538; PubMed=9925787;  
 RA Zhang E., St Charles R., Tulinsky A.;  
 RT "Structure of extracellular tissue factor complexed with factor VIIa  
 RT inhibited with a BPTI mutant.";  
 RL J. Mol. Biol. 285:2089-2104(1999).  
 RN [10]  
 RP STRUCTURE BY NMR OF 105-145.  
 RX MEDLINE=98367502; PubMed=9692950;  
 RA Muranyi A., Finn B.E., Gippert G.P., Forsen S., Stenflo J.,  
 RA Drakenberg T.;  
 RT "Solution structure of the N-terminal EGF-like domain from human  
 RT factor VII.";  
 RL Biochemistry 37:10605-10615(1998).











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GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 15, 2003, 13:24:56 ; Search time 28 Seconds  
(without alignments)  
323.788 Million cell updates/sec

Title: SEQIDL\_MOD

Perfect score: 197

Sequence: 1 ANSFLXLRQGSRLXRCIXX.....XXAKXIFEDVDTLAFWSKH 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues 671580

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_invertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaea.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	151	76.6	456	Q9TTR0	Q9TTR0 canis famil
2	140	71.1	460	Q91WN8	Q91WN8 mus musculus
3	134	68.0	460	Q99PC6	Q99PC6 mus musculus
4	115	58.4	482	Q93207	Q93207 rattus norv
5	101	51.3	481	Q54740	Q54740 mus musculus
6	101	51.3	481	Q99L32	Q99L32 mus musculus
7	101	51.3	481	Q88947	Q88947 mus musculus
8	99	50.3	701	Q96P08	Q96P08 homo sapien
9	95	48.2	469	Q9GMD9	Q9GMD9 ornithorhyn
10	85	43.1	650	Q9NSD0	Q9NSD0 homo sapien
11	85	43.1	650	Q16519	Q16519 homo sapien
12	84	42.6	100	Q15253	Q15253 homo sapien
13	82.5	41.9	542	Q8T613	Q8T613 halocynthia
14	80	40.6	446	Q61109	Q61109 mus musculus
15	80	40.6	456	Q14316	Q14316 homo sapien
16	80	40.6	461	Q95ND7	Q95ND7 pan troglod

17	80	40.6	461	6	Q95ND6
18	78	39.6	138	6	Q28994
19	78	39.6	607	13	Q91001
20	78	39.6	648	6	Q29094
21	73.5	37.3	433	13	Q90YK1
22	73	37.1	49	6	Q95ME8
23	73	37.1	399	11	Q9CQW3
24	72	36.5	98	13	P82807
25	72	36.5	608	13	Q9PTW7
26	66	33.5	25	11	Q9QVH6
27	65	33.0	179	4	Q8TAS3
28	65	33.0	198	11	Q8R182
29	65	33.0	673	11	Q81592
30	64	32.5	674	11	Q99K57
31	63	32.0	678	4	Q14393
32	56.5	28.7	459	10	Q9SE22
33	56.5	28.7	606	10	Q98JG9
34	56.5	28.7	651	10	Q85218
35	55.5	28.2	575	10	Q94E17
36	54.5	27.7	567	10	Q8W4J2
37	54.5	27.7	603	10	Q9LP67
38	53.5	27.2	196	10	Q04284
39	53.5	27.2	431	10	Q94EY5
40	53.5	27.2	506	10	Q9SPF0
41	53.5	27.2	506	10	Q9SE23
42	53.5	27.2	543	10	Q9MB23
43	53.5	27.2	568	10	Q9ASC3
44	53.5	27.2	576	10	Q9C9U4
45	53.5	27.2	576	10	Q9C9U4

## ALIGNMENTS

RESULT 1

Q9TTR0	PRELIMINARY;	PRT;	456 AA.
ID	Q9TTR0		
AC	Q9TTR0		
DT	01-MAY-2000 (TREMREL. 13, Created)		
DT	01-MAY-2000 (TREMREL. 13, Last sequence update)		
DT	01-MAY-2002 (TREMREL. 20, Last annotation update)		
DE	Protein C precursor.		
GN	PROC.		
OS	Canis familiaris (Dog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
OX	NCBI_TaxID=9615;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Leeb T., Kopp T., Deppe A., Breen M., Matis U., Brunnberg L.,		
RA	Brenig B.;		
RT	"Molecular characterization and chromosomal assignment of the canine		
RT	protein C gene."		
RL	Mamm. Genome 10:135-139(1999).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE=99371952; PubMed=10443005;		
RA	Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.;		
RT	"Analysis of canine protein C gene polymorphisms."		
RL	Anim. Genet. 30:237-238(1999).		
CC	- - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE		
CC	TRYPSIN FAMILY.		
DR	EMBL; AJ001979; CAA05126.1; -		
DR	HSSP; P04070; IPCU.		
DR	MEROPS; S01.218; -		
DR	InterPro; IPR000152; Asx_hydroxyl.		
DR	InterPro; IPR001314; Chymotrypsin.		
DR	InterPro; IPR000561; EGF-like.		
DR	InterPro; IPR001881; EGF_Ca.		
DR	InterPro; IPR002383; GLA_blood.		
DR	InterPro; IPR001254; Ser_protease_Try.		
DR	InterPro; IPR000294; VitK_dep_GLA.		
DR	Pfam; PF00008; EGF; 2.		

	Matches	26;	Conservative	7;	Mismatches	11;	Indels	0;	Gaps	0;
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QY	1	ANSFLXXLRGSLXRXICIXXICDFXXAKXIFEDVDDTLAFWSKH	44
		:        :      :      :      :      :	
DB	42	ANSFLEMRPGSLERECMEICDLEEAQEIQFQNVEDTAFWKI	85

  

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RESULT 3
Q99PC6 PRELIMINARY; PRT; 460 AA.
AC Q99PC6;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Anticoagulant protein C.
GN PROC
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Korf I.;
RT "Complete sequence of UC72A01.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
    TRYPSIN FAMILY.
DR EMBL; AF318182; AAK07918.1; -.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR MGD; MG1:97771; Proc.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser.protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla_1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00001; EGF_like; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS02440; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
SQ Hydroxylation; Repeat; Serine protease.
SQ SEQUENCE 460 AA; 51784 MW; 0293BC25E9D3ED16 CRC64;

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Query Match	68.0%;	Score 134;	DB 11;	Length 460;		
Best Local Similarity	56.8%;	Pred. No. 1.4e-14;				
Matches	25;	Conservative	7;	Mismatches 12;	Indels 0;	Gaps 0;

  

QY	1	ANSFLXXLRGSLXRXICIXXICDFXXAKXIFEDVDDTLAFWSKH	44
		:        :      :      :      :      :	
DB	42	ANSFLEMRPGSLERECMEICDLEEAQEIQFQNVEDTAFWKI	85

  

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RESULT 4
Q63207 PRELIMINARY; PRT; 482 AA.
ID Q63207
AC Q63207;

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OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=LIVER;
RA	MEDLINE=98454993; PubMed=9783672;
RX	Heidmann H.H., Kontermann R.E.;
RY	"Cloning and recombinant expression of mouse coagulation factor X.";
RT	Thromb. Res. 92:33-41(1998).
RL	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC	TRYPSIN FAMILY.
DR	EMBL: AJ222677; CAA10933.1; -.
DR	HSP: P00742; IXKA.
DR	MEROPS: S01.216; -.
DR	MGD: MGI:103107; F10.
DR	InterPro: IPR000152; Asx_hydroxyl.
DR	InterPro: IPR001314; Chymotrypsin.
DR	InterPro: IPR000561; EGF-like.
DR	InterPro: IPR000742; EGF_2.
DR	InterPro: IPR001881; EGF_Ca.
DR	InterPro: IPR002383; GLA_blood.
DR	InterPro: IPR001254; Ser_protease_Try.
DR	InterPro: IPR000294; VitK_dep_GLA.
DR	Pfam: PF00008; EGF_2.
DR	Pfam: PF00594; gla; 1.
DR	Pfam: PF00089; trypsin; 1.
DR	PRINTS: PR00722; CHYMOTRYP SIN.
DR	PRINTS: PR00001; GLABLOOD.
DR	SMART: SM00179; EGF_CA; 1.
DR	SMART: SM00001; EGF_like; 1.
DR	SMART: SM00069; GLA; 1.
DR	SMART: SM00020; Tryp_SPC; 1.
DR	PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR	PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR	PROSITE: PS01186; EGF_2; 2.
DR	PROSITE: PS01187; EGF_CA; 1.
DR	PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR	PROSITE: PS00240; TRYP SIN_DOM; 1.
DR	PROSITE: PS00134; TRYP SIN_HIS; UNKNOWN_1.
DR	PROSITE: PS00135; TRYP SIN_SER; 1.
KW	Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid;
KW	Repeat; Serine protease; Signal.
FT	SIGNAL 1 40 POTENTIAL.
FT	CHAIN 41 481 COAGULATION FACTOR X.
SQ	SEQUENCE 481 AA: 53986 MW; CF702DESEF9D7AE CRC64;
Query Match	51.3%; Score 101; DB 11; Length 481;
Best Local Similarity	38.6%; Pred. No. 7.4e-09;
Matches 17; Conservative 10; Mismatches 17; Indels 0; Gaps	
Qy	1 ANSFLLXLQGSLXRXCIXICDFXXAKKXFDDVDTLAFWSKH 44       :    :    :    :    :    :
Dd	41 ANSFFFEFKGNLERECHEICSYEVEIFEDEDKTKETWKY 84       :    :    :    :    :    :
RESULT 6	
Q99L32	PRELIMINARY; PRT; 481 AA.
ID Q99L32	
AC Q99L32;	
DT 01-JUN-2001 (TrEMBLrel. 17, Created)	
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)	
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)	
DE Coagulation factor X.	
GN F10.	
OS Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX NCBI_TaxID=10090;	
RP [1]	
RP SEQUENCE FROM N.A.	
RA Strausberg R.;	
RL Scrausberg (Feb.-2001) to the EMBL/GenBank/DBJ databases.	
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE	
CC TRYPSIN FAMILY.	





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DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 469 AA; 52196 MW; 4C66C230D0758P6A CRC64;

Query Match 48.2%; Score 95; DB 6; Length 469;
Best Local Similarity 40.5%; Pred. No. 7.9e-08;
Matches 17; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANSELXLRGSLRRXCIXXICDFXAXKXIFEDVDDTLAFWS 42
   ||| :||:| | | : | :||| | | | :
DB 41 ANSLFEELKKGNLERECNEETCSYEAREVFEDTDKTNEFMN 82

RESULT 10
Q9NSD0
ID Q9NSD0 PRELIMINARY; PRT; 650 AA.
AC AC
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Protein S precursor.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC NCMLIA; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Dahlbäck B.;
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; X12892; CAA31383.1; -.
DR HSP; P00740; ICFH.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001791; Laminin-G.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00054; laminin_G; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 3.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00282; Lamg; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF-2; 3.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat;
KW Signal.
FT CHAIN 1 15 POTENTIAL.
FT CHAIN 16 650 POTENTIAL.
SQ SEQUENCE 650 AA; 72480 MW; C67345ECE8645174 CRC64;

Query Match 43.1%; Score 85; DB 4; Length 650;
Best Local Similarity 38.6%; Pred. No. 6.1e-06;
Matches 17; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANSELXLRGSLRRXCIXXICDFXAXKXIFEDVDDTLAFWSKH 44
   ||| :||:| | | : | :||| | | | :
DB 16 ANSLFEELKKGNLERECIEELCKNEAREVFENDPETYPKY 59

RESULT 11
Q16519
ID Q16519 PRELIMINARY; PRT; 650 AA.
AC AC
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

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DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Protein S precursor (Fragment).
GN PROS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96313649; PubMed=2944113;
RA Lundwall A., Dackowski W., Cohen E., Shaffer M., Mahr A., Dahlback B.,
RA Stenflo J., Wydro R.;
RT "Isolation and sequence of the cDNA for human protein S, a regulator
RT of blood coagulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:6716-6720(1986).
DR EMBL; M14338; AAA60181.1; -.
DR HSSP; P00740; ICFH.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 3.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00282; LamG; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat;
KW Signal.
FT NON_TER 1 15 POTENTIAL.
FT SIGNAL <1 15 PROTEIN S.
FT CHAIN 16 650
FT SEQUENCE 650 AA; 72462 MW; 9A8C044C503BF474 CRC64;

Query Match 43.1%; Score 85; DB 4; Length 650;
Best Local Similarity 38.6%; Pred. No. 6.1e-06;
Matches 17; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANSLFLXLRQSLRXRCIXXICDFFXAKXIFEDVDDTLAFWSKH 44
||| | :||| | | :| :||| :| | :|
Db 16 ANSLLETKGNLRECEIEELCNKEAREVFENDPETYFPKY 59

RESULT 12
Q15253 PRELIMINARY; PRT; 100 AA.
AC Q15253;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Thrombin precursor (Fragment).
GN F2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87182874; PubMed=3471151;
RA MacGillivray R.T., Irwin D.M., Guinto E.R., Stone J.C.;
RT "Recombinant genetic approaches to functional mapping of thrombin.";
RL Ann. N. Y. Acad. Sci. 485:73-79(1986).
DR EMBL; M33031; AAA60220.1; -.
DR HSSP; P00735; 2PFI.

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DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW Signal.
FT SIGNAL 1 43 POTENTIAL.
FT CHAIN 44 >100 POTENTIAL.
FT NON_TER 100 100
FT SEQUENCE 100 AA; 11302 MW; FD0E5D0174E1F6FE CRC64;

Query Match 42.6%; Score 84; DB 4; Length 100;
Best Local Similarity 36.4%; Pred. No. 1.2e-06;
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANSLFLXLRQSLRXRCIXXICDFFXAKXIFEDVDDTLAFWSKH 44
||| | :||| | | :| :||| :| | :|
Db 44 ANTELEEVKGNLRECEVEETCSYEAEFALESSTATDVFVWAKY 87

RESULT 13
Q8T6I3 PRELIMINARY; PRT; 542 AA.
AC Q8T6I3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Gla-like protein.
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Halocynthia.
OX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang C.-P., Stafford D.W.;
RT "Halocynthia roretzi gla-like protein partial genomic DNA sequence.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF466701; AAL74247.2; -.
DR SEQUENCE 542 AA; 62090 MW; EB9BF13FE42B32FE CRC64;

Query Match 41.9%; Score 82.5; DB 5; Length 542;
Best Local Similarity 34.9%; Pred. No. 1.3e-05;
Matches 15; Conservative 10; Mismatches 17; Indels 1; Gaps 1;

QY 3 SELXLLRQSLRXRCIXXICDFFXAKXIFE-DVDDTLAFWSKH 44
||| | :||| | | :| :||| :| | :|
Db 33 SHFEETQGNLRECEVEELCSFEAREVFETNIQDLNEFWAKY 75

RESULT 14
Q61109 PRELIMINARY; PRT; 446 AA.
AC Q61109;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Coagulation factor VII.
GN F7 OR FVII.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96276538; PubMed=8701412;
RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
RA Castellino F.J.;
RT "Characterization of a cDNA encoding murine coagulation factor VII.";
RL Thromb. Haemost. 75:481-487(1996).
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.

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DR EMBL; U44795; AAC52570.1; -.
DR HSSP; P08709; IFAK.
DR MEROPS; S01.215; -.
DR MGD; MGI:109325; F7.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYPSIN; 1.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;

Query Match 40.6%; Score 80; DB 11; Length 446;
Best Local Similarity 43.9%; Pred. No. 2.9e-05;
Matches 18; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANSFLXLRQGSRLXRCIXXICDFXXAKXIFEDVDDTLAFW 41
DB 42 ANSLEELWPGSLERECNEEQCSFEAREIFKSPERTKQFW 82

RESULT 15
Q14316
ID Q14316 PRELIMINARY; PRT; 456 AA.
AC Q14316;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-AUG-1999 (TRENBLrel. 11, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, christmas
DE disease, HAEMOPHILIA B)) (Factor IX).
GN F9 OR FACTOR IX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=88327116; PubMed=3416069;
RA Reitsma P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,
RA Briet E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; AL033403; CAA21954.1; -.
DR EMBL; X55008; CAB38245.2; -.

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DR HSSP; P00740; ICFH.
DR MEROPS; S01.214; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYPSIN; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
KW Serine protease.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match 40.6%; Score 80; DB 4; Length 456;
Best Local Similarity 37.1%; Pred. No. 3e-05;
Matches 13; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 10 QGSLXRCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
DB 52 QGNLERECNEEKCSFEAREVEFENTERTEFWKQY 86

Search completed: May 15, 2003, 13:28:11
Job time : 31 secs

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OM protein - protein search, using sw model

Run on: May 15, 2003, 13:26:41 ; Search time 15 Seconds  
(without alignments)  
86.307 Million cell updates/sec

Title: SEQID1\_MOD  
Perfect score: 197  
Sequence: 1 ANSFLXLRQSLKRXKICIX.....XXAKXIFEDVDTLAFWSKH 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCUTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the total being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	179	90.9	44	3	US-08-955-636-24
2	176	89.3	44	3	US-08-955-636-35
3	173	87.8	44	3	US-08-955-636-20
4	170	86.3	44	3	US-08-955-636-21
5	168	85.3	44	3	US-08-955-636-19
6	168	85.3	44	3	US-08-955-636-22
7	166	81.2	44	3	US-08-955-636-1
8	160	81.2	44	3	US-08-955-636-25
9	160	81.2	45	2	US-08-965-832-2
10	160	81.2	419	2	US-08-295-411-1
11	160	81.2	419	2	US-08-955-471-1
12	160	81.2	419	2	US-08-667-570A-3
13	160	81.2	419	5	PCR-US92-10242-1
14	160	81.2	460	2	US-08-756-506-2
15	160	81.2	460	2	US-08-756-506-4
16	160	81.2	460	6	5270178-13
17	160	81.2	460	6	5270178-14
18	160	81.2	460	6	5270178-15
19	160	81.2	460	6	5270178-16
20	160	81.2	461	6	5225537-2
21	160	81.2	461	6	5270178-17
22	160	81.2	461	6	5270178-18
23	160	81.2	461	6	5460953-3
24	147	74.6	42	2	US-08-745-254A-2
25	147	74.6	461	6	5270178-2
26	143	72.6	41	1	US-08-229-280-5
27	129	65.5	409	4	US-09-065-872-2

28	129	65.5	409	4	US-09-667-570A-2	Sequence 2, Appl1
29	129	65.5	410	4	US-09-065-872-1	Sequence 1, Appl1
30	129	65.5	410	4	US-09-667-570A-1	Sequence 1, Appl1
31	117	59.4	44	3	US-08-955-636-23	Sequence 23, Appl1
32	116	58.9	44	3	US-08-955-636-23	Sequence 2, Appl1
33	114	57.9	139	1	US-08-330-978-2	Sequence 2, Appl1
34	114	57.9	139	1	US-08-474-042-2	Sequence 2, Appl1
35	114	57.9	139	1	US-08-484-558-2	Sequence 2, Appl1
36	114	57.9	139	1	US-08-774-592-2	Sequence 2, Appl1
37	114	57.9	437	1	US-08-487-037-2	Sequence 2, Appl1
38	114	57.9	437	1	US-08-487-037-3	Sequence 3, Appl1
39	114	57.9	487	1	US-08-469-486-53	Sequence 53, Appl1
40	114	57.9	487	2	US-08-469-658-53	Sequence 53, Appl1
41	114	57.9	488	1	US-08-487-037-1	Sequence 2, Appl1
42	114	57.9	492	1	US-08-469-486-2	Sequence 2, Appl1
43	114	57.9	492	2	US-08-469-658-2	Sequence 2, Appl1
44	110	55.8	448	1	US-08-295-411-3	Sequence 3, Appl1
45	110	55.8	448	2	US-08-955-471-3	Sequence 3, Appl1

## ALIGNMENTS

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RESULT 1
US-08-955-636-24
; Sequence 24, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelissen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa-gamma carboxylutamic acid or glutamic acid
US-08-955-636-24

Query Match          90.9%  Score 179;  DB 3;  Length 44;
Best Local Similarity 100.0%  Pred. NO. 1.2e-23;
Matches 44;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      1 ANSFLXLRQSLKRXKICIXCDPFXAKXIFEDVDTLAFWSKH 44
DB      1 ANSFLXLRQSLKRXKICIXCDPFXAKXIFEDVDTLAFWSKH 44

RESULT 2
US-08-955-636-35
; Sequence 35, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelissen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

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NAME/KEY: MOD\_RES  
LOCATION: (0)...(0)  
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-35

Query Match 89.3%; Score 176; DB 3; Length 44;  
Best Local Similarity 97.7%; Pred. No. 3.8e-23;  
Matches 43; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ANSFLXLRGSLRXRCIXXICDFXXAKXIFEDVDTLAFWSKH 44  
DB 1 ANSFLXLRGSLRXRCIXXICDFXXAKXIFEDVDTLAFWSKH 44

RESULT 3  
US-08-955-636-20  
Sequence 20, Application US/08955636A  
Patent No. 6017882  
GENERAL INFORMATION:

APPLICANT: Nelstuen, Gary  
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
FILE REFERENCE: 09531/002001  
CURRENT APPLICATION NUMBER: US/08/955,636A  
CURRENT FILING DATE: 1997-10-23  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 20

LENGTH: 44  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:

NAME/KEY: MOD\_RES  
LOCATION: (0)...(0)  
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-20

Query Match 87.8%; Score 173; DB 3; Length 44;  
Best Local Similarity 97.7%; Pred. No. 1.2e-22;  
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ANSFLXLRGSLRXRCIXXICDFXXAKXIFEDVDTLAFWSKH 44  
DB 1 ANSFLXLRGSLRXRCIXXICDFXXAKXIFEDVDTLAFWSKH 44

RESULT 4  
US-08-955-636-21

Sequence 21, Application US/08955636A  
Patent No. 6017882  
GENERAL INFORMATION:

APPLICANT: Nelstuen, Gary  
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
FILE REFERENCE: 09531/002001  
CURRENT APPLICATION NUMBER: US/08/955,636A  
CURRENT FILING DATE: 1997-10-23  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 21

LENGTH: 44  
TYPE: PRT

ORGANISM: Homo sapiens  
FEATURE:

NAME/KEY: MOD\_RES  
LOCATION: (0)...(0)  
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-21

Query Match 86.3%; Score 170; DB 3; Length 44;  
Best Local Similarity 95.5%; Pred. No. 4e-22;  
Matches 42; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ANSFLXLRGSLRXRCIXXICDFXXAKXIFEDVDTLAFWSKH 44  
DB 1 ANSFLXLRGSLRXRCIXXICDFXXAKXIFEDVDTLAFWSKH 44

RESULT 5  
US-08-955-636-19  
Sequence 19, Application US/08955636A  
Patent No. 6017882  
GENERAL INFORMATION:

APPLICANT: Nelstuen, Gary  
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
FILE REFERENCE: 09531/002001  
CURRENT APPLICATION NUMBER: US/08/955,636A  
CURRENT FILING DATE: 1997-10-23  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 19

LENGTH: 44  
TYPE: PRT

ORGANISM: Homo sapiens  
FEATURE:

NAME/KEY: MOD\_RES  
LOCATION: (0)...(0)  
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-19

Query Match 85.3%; Score 168; DB 3; Length 44;  
Best Local Similarity 95.5%; Pred. No. 8.9e-22;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ANSFLXLRGSLRXRCIXXICDFXXAKXIFEDVDTLAFWSKH 44  
DB 1 ANSFLXLRHSLRXRCIXXICDFXXAKXIFEDVDTLAFWSKH 44

RESULT 6  
US-08-955-636-22

Sequence 22, Application US/08955636A  
Patent No. 6017882  
GENERAL INFORMATION:

APPLICANT: Nelstuen, Gary  
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
FILE REFERENCE: 09531/002001  
CURRENT APPLICATION NUMBER: US/08/955,636A  
CURRENT FILING DATE: 1997-10-23  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 22

LENGTH: 44  
TYPE: PRT

ORGANISM: Homo sapiens  
FEATURE:

NAME/KEY: MOD\_RES  
LOCATION: (0)...(0)  
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-22

Query Match 85.3%; Score 168; DB 3; Length 44;  
Best Local Similarity 95.5%; Pred. No. 8.9e-22;  
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ANSFLXLRGSLRXRCIXXICDFXXAKXIFEDVDTLAFWSKH 44  
DB 1 ANSFLXLRDSSLRXRCIXXICDFXXAKXIFEDVDTLAFWSKH 44

RESULT 7  
US-08-955-636-1  
Sequence 1, Application US/08955636A  
Patent No. 6017882

GENERAL INFORMATION:  
APPLICANT: Nelsaetuen, Gary  
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
FILE REFERENCE: 09531/002001  
CURRENT APPLICATION NUMBER: US/08/955,636A  
CURRENT FILING DATE: 1997-10-23  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 1  
LENGTH: 44  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (0)...(0)  
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-1

Query Match 81.2%; Score 160; DB 3; Length 44;  
Best Local Similarity 90.9%; Pred. No. 2e-20;  
Matches 40; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 ANSFLXXLRQSLXRXICIXXICDFXXAKXIFEDVDDTLAFWSKH 44  
DB 1 ANSFLXXLRHSSILXRXICIXXICDFXXAKXIFQVDDTLAFWSKH 44

RESULT 8  
US-08-955-636-25  
Sequence 25, Application US/08955636A  
Patent No. 6017882  
GENERAL INFORMATION:  
APPLICANT: Nelsaetuen, Gary  
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT  
FILE REFERENCE: 09531/002001  
CURRENT APPLICATION NUMBER: US/08/955,636A  
CURRENT FILING DATE: 1997-10-23  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 25  
LENGTH: 44  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (0)...(0)  
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid  
US-08-955-636-25

Query Match 81.2%; Score 160; DB 3; Length 44;  
Best Local Similarity 93.2%; Pred. No. 2e-20; 3; Indels 0; Gaps 0;  
Matches 41; Conservative 0; Mismatches 3; Indels 0;

OY 1 ANSFLXXLRQSLXRXICIXXICDFXXAKXIFEDVDDTLAFWSKH 44  
DB 1 ANSFLXXLRHSSILXRXICIXXICDFXXAKXIFEDVDDTLAFWSKH 44

RESULT 9  
US-08-965-832-2  
Sequence 2, Application US/08965832  
Patent No. 5847085  
GENERAL INFORMATION:  
APPLICANT: CHARLES T. ESKOW AND MIKHAIL D. SMIRNOV  
TITLE OF INVENTION: Modified Protein C  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center, 1201 West  
STREET: Peachtree Street  
CITY: Atlanta

STATE: GA  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/965,832  
FILING DATE: 7-NOV-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/745,254  
FILING DATE: 8-NOV-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/053,768  
FILING DATE: 25-JUL-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OARF 165/167  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-873-8794  
TELEFAX: (404)-873-8795  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY:  
LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29  
OTHER INFORMATION: /note="where Xaa means gamma  
OTHER INFORMATION: carboxyglutamic acid"  
FEATURE:  
NAME/KEY:  
LOCATION:  
OTHER INFORMATION: /note="partial sequence of human protein C"

US-08-965-832-2

Query Match 81.2%; Score 160; DB 2; Length 45;  
Best Local Similarity 90.9%; Pred. No. 2.1e-20;  
Matches 40; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 ANSFLXXLRQSLXRXICIXXICDFXXAKXIFEDVDDTLAFWSKH 44  
DB 1 ANSFLXXLRHSSILXRXICIXXICDFXXAKXIFQVDDTLAFWSKH 44

RESULT 10  
US-08-295-411-1  
Sequence 1, Application US/08295411  
Patent No. 5679639  
GENERAL INFORMATION:  
APPLICANT: Griffin, John H.  
APPLICANT: Meesters, Rolf M.  
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESSEE: Research Institute  
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,471
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSR163.OCL
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..157
OTHER INFORMATION: /note= "Protein C Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 158..169
OTHER INFORMATION: /note= "Protein C Activation"
OTHER INFORMATION: Peptide"
FEATURE:
NAME/KEY: Region
LOCATION: 170..419
OTHER INFORMATION: /note= "Protein C Heavy Chain"
US-08-955-471-1

Query Match      81.2%; Score 160; DB 2; Length 419;
Best Local Similarity 70.5%; Pred. No. 2,7e-19;
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

OY    1 ANSFLXLRQGSILKRCIXIXICDFFXAKXIEDVDVDTLAFWSKH 44
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DB    1 ANSFLEELRHSSLERECIEICDFEAEKEIFQWDDTLAFWSKH 44

RESULT 12
US-09-667-570A-3
Sequence 3, Application US/09667570A
Patent No. 6436397
GENERAL INFORMATION:
APPLICANT: Baker, Jeffrey C
APPLICANT: Carlson, Andrew D
APPLICANT: Huang, Lihua
APPLICANT: Shetiga, Theodore A
TITLE OF INVENTION: Improved Methods for Processing Activated Protein C
FILE REFERENCE: X-11796A
CURRENT APPLICATION NUMBER: US/09/667,570A
CURRENT FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/045,255
PRIORITY FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-09-667-570A-3

Query Match      81.2%; Score 160; DB 4; Length 419;
Best Local Similarity 70.5%; Pred. No. 2,7e-19;

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Matches 31: Conservative 2: Mismatches 11: Indels 0: Gaps 0:

QY 1 ANSFLXLRHSSLRRCIEICDFEAKEIFQVNDTLAFWSKH 44  
DB 1 ANSFLXLRHSSLRRCIEICDFEAKEIFQVNDTLAFWSKH 44

RESULT 13

PCT-US92-10242-1  
Sequence 1, Application PC/TUS9210242

GENERAL INFORMATION:

APPLICANT: Griffon, John H.

APPLICANT: Meesters, Rolf

TITLE OF INVENTION: Serine Protease-Derived Polypeptides and

TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods

TITLE OF INVENTION: for Inhibiting Coagulation

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Office of Patent Counsel, The Scripps

ADDRESSEE: Research Institute

STREET: 10666 North Torrey Pines Road, TPC 8

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/10242

FILING DATE: 19921118

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/793,989

FILING DATE: 18-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: SCRO472P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-554-2937

TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 419 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: Region

LOCATION: 1..157

OTHER INFORMATION: /note- "Protein C Light Chain"

FEATURE:

NAME/KEY: Region

LOCATION: 170..419

OTHER INFORMATION: /note- "Protein C Heavy Chain"

PCT-US92-10242-1

Query Match

Best Local Similarity 81.2%; Score 160; DB 5: Length 419;

DB 1 ANSFLXLRHSSLRRCIEICDFEAKEIFQVNDTLAFWSKH 44

QY 1 ANSFLXLRHSSLRRCIEICDFEAKEIFQVNDTLAFWSKH 44  
DB 43 ANSFLXLRHSSLRRCIEICDFEAKEIFQVNDTLAFWSKH 86

RESULT 14

US-08-756-506-2  
Sequence 2, Application US/08756506

Patent No. 5905185

GENERAL INFORMATION:

APPLICANT: Garner, Ian

APPLICANT: Cottingham, Ian R.

APPLICANT: Temperley, Simon M.

APPLICANT: Foster, Donald C.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Prunkard, Donna E.

TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC

TITLE OF INVENTION: ANIMALS

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics, Inc.

STREET: 1201 Eastlake Avenue East

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/756,506

FILING DATE: 800

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Sawislak, Deborah A

REGISTRATION NUMBER: 37,438

REFERENCE/DOCKET NUMBER: 95-28

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6672

TELEFAX: 206-442-6678

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 460 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-756-506-2

Query Match

Best Local Similarity 81.2%; Score 160; DB 2: Length 460;

Matches 31: Conservative 2: Mismatches 11: Indels 0: Gaps 0:

QY 1 ANSFLXLRHSSLRRCIEICDFEAKEIFQVNDTLAFWSKH 44  
DB 43 ANSFLXLRHSSLRRCIEICDFEAKEIFQVNDTLAFWSKH 86

RESULT 15  
US-08-756-506-4  
Sequence 4, Application US/08756506

Patent No. 5905185

GENERAL INFORMATION:

APPLICANT: Garner, Ian

APPLICANT: Cottingham, Ian R.

APPLICANT: Temperley, Simon M.

APPLICANT: Foster, Donald C.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Prunkard, Donna E.

TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC

TITLE OF INVENTION: ANIMALS

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics, Inc.

STREET: 1201 Eastlake Avenue East  
City: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/756,506  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Sawislak, Deborah A  
REGISTRATION NUMBER: 37,438  
REFERENCE/DOCKET NUMBER: 95-28  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6672  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ. ID NO.: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 460 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-756-506-4

	Query Match	81.2%	Score 160;	DB 2;	Length 460;
	Best Local Similarity	70.5%	Pred. No. 3,le-19;		
	Matches	31;	Conservative	2; Mismatches	11; Indels
					Gaps 0;
QY	1 ANSFLAAROGSLAKXCIXXICDFEAXKXIIFDVDDITLAFMSKH	44			
Db	43 ANSFLEEDRHSHSLERCEIEICDPEAEKEIFONVDITLAFMSKH	86			

Search completed: May 15, 2003, 13:28:55  
Job time : 16 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	Length				
1	179	90.9	419	9	US-10-182-263-6		Sequence 6, Appl1
2	174	88.3	419	9	US-10-182-263-3		Sequence 3, Appl1
3	174	88.3	419	9	US-10-182-263-4		Sequence 4, Appl1
4	174	88.3	419	9	US-10-182-263-5		Sequence 5, Appl1
5	160	81.2	419	9	US-10-182-263-1		Sequence 1, Appl1
6	160	81.2	419	9	US-09-978-917A-4		Sequence 4, Appl1
7	160	81.2	461	9	US-10-182-263-2		Sequence 2, Appl1
8	160	81.2	461	9	US-09-978-917A-2		Sequence 2, Appl1
9	99	50.3	465	9	US-10-017-122-2		Sequence 2, Appl1
10	96	48.7	406	9	US-10-109-498-1		Sequence 1, Appl1
11	84.5	42.9	96	9	US-09-759-130B-313		Sequence 313, App
12	84.5	42.9	96	9	US-10-189-123-43		Sequence 43, Appl
13	84.5	42.9	209	9	US-09-759-130B-312		Sequence 312, App
14	84.5	42.9	209	9	US-10-189-123-42		Sequence 42, Appl
15	84.5	42.9	226	9	US-09-759-130B-310		Sequence 310, App
16	84.5	42.9	226	9	US-10-189-123-40		Sequence 40, Appl
17	80	40.6	415	10	US-09-118-748-5		Sequence 2, Appl1
18	80	40.6	461	9	US-10-132-629-5		Sequence 5, Appl1
19	80	40.6	461	10	US-09-684-901-3		Sequence 3, Appl1

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; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

Query Match      88.3%; Score 174; DB 9; Length 419;
Best Local Similarity 77.3%; Pred. No. 3.8e-21;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXXLRGSLXRCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLRLRHGSLERCIEICDFEAKEIFEDVDDTLAFWSKH 44

RESULT 3
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-4

Query Match      88.3%; Score 174; DB 9; Length 419;
Best Local Similarity 77.3%; Pred. No. 3.8e-21;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXXLRGSLXRCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLRLRHGSLERCIEICDFEAKEIFEDVDDTLAFWSKH 44

RESULT 4
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-5

Query Match      88.3%; Score 174; DB 9; Length 419;
Best Local Similarity 77.3%; Pred. No. 3.8e-21;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXXLRGSLXRCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLRLRHGSLERCIEICDFEAKEIFEDVDDTLAFWSKH 44

RESULT 5
US-10-182-263-1
; Sequence 1, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-1

Query Match      81.2%; Score 160; DB 9; Length 419;
Best Local Similarity 70.5%; Pred. No. 8.6e-19;
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANSFLXXLRGSLXRCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLRLRHGSLERCIEICDFEAKEIFQNVDDTLAFWSKH 44

RESULT 6
US-09-978-917A-4
; Sequence 4, Application US/09978917A
; Publication No. US20030027299A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219us310 - protein C
; CURRENT APPLICATION NUMBER: US/09/978,917A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-917A-4

Query Match      81.2%; Score 160; DB 9; Length 419;
Best Local Similarity 70.5%; Pred. No. 8.6e-19;
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANSFLXXLRGSLXRCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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US-10-017-122-2  
; Sequence 2, Application US/100171122

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APPLICANT: Myers, Paul S  
APPLICANT: Leiby, Kevin R  
APPLICANT: Wrighton, Nicolas  
APPLICANT: Goodearl, Andrew  
APPLICANT: Holtzman, Douglas A  
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
TITLE OF INVENTION: USES  
FILE REFERENCE: MPI00-5350MNM  
CURRENT APPLICATION NUMBER: US/09/759,130B  
CURRENT FILING DATE: 2002-09-16  
PRIOR APPLICATION NUMBER: US 09/479,249  
PRIOR FILING DATE: 2000-01-07  
PRIOR APPLICATION NUMBER: US 09/559,497  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: US 09/578,063  
PRIOR FILING DATE: 2000-05-24  
PRIOR APPLICATION NUMBER: US 09/333,159  
PRIOR FILING DATE: 1999-06-14  
PRIOR APPLICATION NUMBER: US 09/596,194  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/342,364  
PRIOR FILING DATE: 1999-06-29  
PRIOR APPLICATION NUMBER: US 09/608,452  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/393,996  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US 09/602,871  
PRIOR FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: US 09/420,707  
PRIOR FILING DATE: 1999-10-19  
NUMBER OF SEQ ID NOS: 460  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 313  
LENGTH: 96  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-759-130B-313

Query Match 42.9%; Score 84.5; DB 9; Length 96;  
Best Local Similarity 38.6%; Pred. No. 9e-07;  
Matches 17; Conservative 8; Mismatches 18; Indels 1; Gaps 1;

Qy 2 NSF-LXXLRQSLRXKXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44  
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Db 36 NRFDELFPGNLERECNEELCNTEAREIFVDEKTIAFWQY 79

RESULT 12  
US-10-189-123-43  
Sequence 43, Application US/10189123  
Publication No. US20030082586A1  
GENERAL INFORMATION:  
APPLICANT: KIRST, Susan J.  
APPLICANT: HOLTZMAN, Douglas A.  
APPLICANT: FRASER, Christopher C.  
APPLICANT: SHARP, John D.  
APPLICANT: BARNES, Thomas S.  
TITLE OF INVENTION: ANTIBODIES HAVING DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
FILE REFERENCE: 10147-1103  
CURRENT APPLICATION NUMBER: US/10/189,123  
CURRENT FILING DATE: 2002-07-02  
PRIOR APPLICATION NUMBER: US 09/596,194  
PRIOR FILING DATE: 2000-06-16  
PRIOR APPLICATION NUMBER: US 09/342,364  
PRIOR FILING DATE: 1999-06-29  
NUMBER OF SEQ ID NOS: 100  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 43  
LENGTH: 96  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-189-123-43

Query Match 42.9%; Score 84.5; DB 9; Length 96;  
Best Local Similarity 38.6%; Pred. No. 9e-07;  
Matches 17; Conservative 8; Mismatches 18; Indels 1; Gaps 1;

Qy 2 NSF-LXXLRQSLRXKXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44  
| | | | | : | | | | : | | | | : | | | | :  
Db 36 NRFDELFPGNLERECNEELCNTEAREIFVDEKTIAFWQY 79

RESULT 13  
US-09-759-130B-312  
Sequence 312, Application US/09759130B  
Publication No. US2003002279A1  
GENERAL INFORMATION:  
APPLICANT: Millennium Pharmaceuticals, Inc.  
APPLICANT: McCarthy, Sean A  
APPLICANT: Fraser, Christopher C  
APPLICANT: Sharp, John D  
APPLICANT: Barnes, Thomas S  
APPLICANT: Kirst, Susan J  
APPLICANT: Mackay, Charles R  
APPLICANT: Myers, Paul S  
APPLICANT: Leiby, Kevin R  
APPLICANT: Wrighton, Nicolas  
APPLICANT: Goodearl, Andrew  
APPLICANT: Holtzman, Douglas A  
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
TITLE OF INVENTION: USES  
FILE REFERENCE: MPI00-5350MNM  
CURRENT APPLICATION NUMBER: US/09/759,130B  
CURRENT FILING DATE: 2002-09-16  
PRIOR APPLICATION NUMBER: US 09/479,249  
PRIOR FILING DATE: 2000-01-07  
PRIOR APPLICATION NUMBER: US 09/559,497  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: US 09/578,063  
PRIOR FILING DATE: 2000-05-24  
PRIOR APPLICATION NUMBER: US 09/333,159  
PRIOR FILING DATE: 1999-06-14  
PRIOR APPLICATION NUMBER: US 09/596,194  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/342,364  
PRIOR FILING DATE: 1999-06-29  
PRIOR APPLICATION NUMBER: US 09/608,452  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/393,996  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US 09/602,871  
PRIOR FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: US 09/420,707  
PRIOR FILING DATE: 1999-10-19  
NUMBER OF SEQ ID NOS: 460  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 312  
LENGTH: 209  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-759-130B-312

Query Match 42.9%; Score 84.5; DB 9; Length 209;  
Best Local Similarity 38.6%; Pred. No. 2.1e-06;  
Matches 17; Conservative 8; Mismatches 18; Indels 1; Gaps 1;

Qy 2 NSF-LXXLRQSLRXKXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44  
| | | | | : | | | | : | | | | : | | | | :  
Db 36 NRFDELFPGNLERECNEELCNTEAREIFVDEKTIAFWQY 79

RESULT 14  
US-10-189-123-42  
Sequence 42, Application US/10189123

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; Publication No. US20030082586A1
; GENERAL INFORMATION:
; APPLICANT: KIRST, Susan J.
; APPLICANT: HOLTZMAN, Douglas A.
; APPLICANT: FRASER, Christopher C.
; APPLICANT: SHARP, John D.
; APPLICANT: BARNES, Thomas S.
; TITLE OF INVENTION: ANTIBODIES HAVING DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: 10147-1103
; CURRENT APPLICATION NUMBER: US/10/189,123
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-189-123-42

Query Match      42.9%; Score 84.5; DB 9; Length 209;
Best Local Similarity 38.6%; Pred No. 2.1e-06;
Matches 17; Conservative 8; Mismatches 18; Indels 1; Gaps 1;

QY  2 NSF-LXXLRQSLRXRCIXXCDFXXAKXIFEDVDVDTLAFWSKH 44
    | | | | | | | | | | | | | | | | | | | | | | | |
Db  36 NRRDLELFTPGNLERECNEELCNYEAREIFVDEDKTIAFWQY 79

RESULT 15
US-09-759-130B-310
; Sequence 310, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Sharp, John D.
; APPLICANT: Barnes, Thomas S.
; APPLICANT: Kirst, Susan J.
; APPLICANT: Mackay, Charles R.
; APPLICANT: Myers, Paul S.
; APPLICANT: Leiby, Kevin R.
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23

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; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-310

Query Match      42.9%; Score 84.5; DB 9; Length 226;
Best Local Similarity 38.6%; Pred No. 2.3e-06;
Matches 17; Conservative 8; Mismatches 18; Indels 1; Gaps 1;

QY  2 NSF-LXXLRQSLRXRCIXXCDFXXAKXIFEDVDVDTLAFWSKH 44
    | | | | | | | | | | | | | | | | | | | | | | | |
Db  53 NRRDLELFTPGNLERECNEELCNYEAREIFVDEDKTIAFWQY 96

Search completed: May 15, 2003, 13:29:21
Job time : 20 secs

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